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H0617: 2, L0769: 2,	0771: 2, L0662: 2,	L0649: 2, L0806: 2,	,0438: 2, S0328: 2,	H0694: 2, L0439: 2,	,0751: 2, L0780: 2,	.0592: 2, L0608: 2,	H0650: 1, L0785: 1,	H0638: 1, H0208: 1,	10132: 1, H0370: 1,	H0438: 1, H0592: 1,	H0599: 1, H0421: 1,	H0596: 1, T0110: 1,	H0597: 1, L0163: 1,	.0455: 1, L0456: 1,	H0124: 1, S0366: 1,	H0040: 1, H0551: 1,	H0059: 1, S0386: 1,	F0042: 1, H0334: 1,	S0144: 1, L0763: 1,	L0770: 1, L0761: 1,	L0772: 1, L0764: 1,	L0774: 1, L0659: 1,	L0789: 1, H0144: 1,	H0520: 1, H0547: 1,	H0658: 1, H0670: 1,	S0378: 1, H0521: 1,	L0749: 1, S0011: 1 and	H0653: 1.	AR089: 2, AR061: 2
Phe-361 to Asp-367, H			_	. /				<u> </u>	S	<u>. i. i. i.</u>							<u>.</u>												Pro-14 to Thr-20,
																	•												1522
	-	-			-		•		•																				1 - 630
-															_	•													622
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	- 1-12												-					-											HWLLR80
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S0358: 1, H0370: 1, H0253: 1, H0040: 1, H0547: 1, L0601: 1 and S0196: 1.	AR089: 23, AR061: 12 L0731: 6, L0766: 5, L0759: 5, L0471: 2, H0038: 2, L0748: 2, L0740: 2, L0748: 2, L0590: 2, S0360: 1, H0596: 1, H0046: 1, L0483: 1, H0644: 1, H0616: 1, H0509: 1, H0647: 1, S0210: 1, L0648: 1, L0363: 1, L06774: 1, L0775: 1, L0666: 1, L0664: 1, S0126: 1, H0672: 1, L0744: 1, L0593: 1, L0744: 1, L0593: 1, L0595: 1, H0665: 1 and S0194: 1.	AR061: 1, AR089: 1 L0748: 8, L0769: 7, L0758: 7, L0749: 5, H0135: 4, S0418: 3, S0358: 3, H0618: 3, H0424: 3, H0529: 3,
Glu-44 to Gly-50, Pro-104 to Gly-111, Gly-127 to Leu-132, Asn-146 to Asp-151, Asn-165 to Glu-170, Ser-194 to Asp-202.	Ile-11 to Glu-19.	
	1523	1524
	76 - 519	3 - 1595
	623	624
	932577	942872
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	613	614

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HU252: 1, 10000: 1,	HU213: 1, HU303: 1,	H0644: 1, H0673: 1,	H0068: 1, H0038: 1,	H0040: 1, H0551: 1,	H0413: 1, H0100: 1,	H0131: 1, S0150: 1,	S0144: 1, S0422: 1,	L0369: 1, L0763: 1,	L0646: 1, L0643: 1,	L0645: 1, L0773: 1,	L0662: 1, L0768: 1,	L0364: 1, L0650: 1,	L0774: 1, L0775: 1,	L0378: 1, L0776: 1,	L0657: 1, L0659: 1,	L0783: 1, L0666: 1,	L0665: 1, S0428: 1,	H0144: 1, H0520: 1,	H0519: 1, H0435: 1,	H0658: 1, H0666: 1,	H0518: 1, H0521: 1,	H0696: 1, L0609: 1,	S3014: 1, S0027: 1,	L0741: 1, L0744: 1,	L0754: 1, L0752: 1,	L0731: 1, L0759: 1,	L0596: 1, H0665: 1,	H0423: 1 and S0446: 1.	AR089: 2 AR061: 1
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H0624: 2 and S0031: 1.	S0001: 1, S0045: 1 and (20216: 1.)		L0777: 20, L0439: 11, L0747: 10, S0360: 6,	L0766: 6, L0758: 6,	7: 5, H0521: 5,	8: 3, S0330: 3,	L0752: 3, L0755: 3,	9: 3, S0358: 2,	;1: 2, S0003: 2,	4: 2, H0068: 2,	L0764: 2, L0662: 2,	5: 2, L0666: 2,	L0665: 2, H0648: 2,	.0: 2, L0751: 2,	L0749: 2, L0750: 2,	11: 2, L0757: 2,	11: 2, L0596: 2,	31: 2, L0362: 2,)2: 2, H0542: 2,	S0040: 1, H0650: 1,	H0657: 1, S0282: 1,	H0580: 1, H0393: 1,	86: 1, H0574: 1,	86: 1, L0586: 1,	H0013: 1, L0021: 1,
90H	Asn-44 to Ala-51. S0001: S0216: 1	Phe-2 to Ser-8, Glu-58 to Gln-63, Asn-74 to Leu-81.		F076	L071,	H003	L075	L059	H058	S021	9L01	T065	990T	L074	L074	L073	S003	L058	S019	S004	H06	H05	H05	H04	H00
	1526 Asn-44	1788 Phe-2 to Ser-8, Glu-58 to Gln-Asn-74 to Leu-	1527										-												
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H0036: 1, H0318: 1, L0563: 1, H0545: 1, S0051: 1, T0010: 1, H01375: 1, H0188: 1, H0119: 1, H0040: 1, H0591: 1, H0040: 1, H0616: 1, T0067: 1, L0369: 1, L0763: 1, L076: 1, L0772: 1, L0389: 1, L0774: 1, L0775: 1, L0375: 1, L0775: 1, L0538: 1, L0776: 1, L059: 1, L0776: 1, L058: 1, L0776: 1, H0558: 1, H0435: 1, H0658: 1, H0445: 1, L0756: 1, L0779: 1, H0444: 1, H0445: 1, L0366: 1,		AR061: 0, AR089: H0305: 3, L0105: 3,
	Glu-1 to Glu-7, Ile-14 to Thr-19.	Cys-32 to Cys-39, Glu-47 to Pro-52,
	1789	1528
÷	241 - 26	489 - 1295
	886	628
	959570	992999
		HBXF175
		618

			147781, 172471, 182381
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L0608: 3, H0624: 1, H0589: 1, H0438: 1, H0250: 1, S0050: 1, H0135: 1, S0144: 1, H0689: 1 and S0028: 1.			AR089: 9, AR061: 5 H0584: 5, H0599: 5, H0556: 4, H0124: 4, H0559: 3, H0622: 3, H0341: 2, H0125: 2, S0045: 2, H0620: 2, H0024: 2, T0042: 2, L0665: 2, H0144: 2, H0265: 1, S6024: 1,
7. 0. E. 4. 0. E. 2. E.	Asp-72 to Glu-78, Ser-103 to Glu-110, Lys-112 to His-117.	Lys-42 to Pro-47, Ser-93 to Ala-99, Asp-118 to Arg-125, Arg-158 to Asn-168, Ala-251 to Val-263, His-287 to Tvr-292.	Glu-302 to Gln-307. Gly-1 to Ser-8, Arg-10 to Ser-15, Leu-17 to Gly-22, Lys-115 to Ala-130, Tyr-149 to Gly-156, Asn-181 to Glu-190, Glu-252 to Glu-257, Ser-339 to Asp-347, Leu-356 to Leu-361,
1790	1791	1792	1529
489 - 1295	30 - 647	748 - 1923	1 - 1437
890	168	892	629
566768	847653	847655	913938
			HELGM94 913938
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H0583: 1, H0208: 1, S0046: 1, H0393: 1, S0278: 1, H0549: 1, H0550: 1, H0438: 1, H0586: 1, H0486: 1, H0618: 1, H0253: 1, H0009: 1, H0687: 1, H0031: 1, H0424: 1, H0116: 1, H0494: 1, H0132: 1, H0131: 1, H0132: 1, H0131: 1, H0130: 1, L0662: 1, L0803: 1, S0126: 1, S0216: 1, S0126: 1, H0518: 1, S0152: 1, S0118: 1, S0152: 1,	AR089: 15, AR061: 1 T0109: 1, H0013: 1, H0375: 1, H0509: 1, H0519: 1, H0690: 1, S0152: 1 and L0485: 1.	AR089: 4, AR061: 1 L0803: 5, L0731: 4, L0662: 3, L0665: 3, S0276: 3, H0486: 2, H0575: 2, H0318: 2, L0794: 2, L0805: 2,
Ser-387 to Lys-395, Thr-470 to Ile-476.	Gly-26 to Val-70, Ser-199 to Arg-204.	Pro-7 to Arg-12, Leu-32 to His-52, Tyr-54 to Asp-69, Pro-74 to Gly-92, Glu-99 to Arg-125, Asp-130 to Glu-142,
	1530	1531
	3 - 824	68 - 2323
	630	631
	923110	1219455
	HLDQ52	HAJAW40
	620	621

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L0776: 2, L0809: 2,	.0740: 2, L0759: 2,	592: 2, H0624: 1,	L0448: 1, H0341: 1,	82: 1, H0663: 1,	S0360: 1, H0580: 1,	.0468: 1, H0587: 1,	H0427: 1, S0010: 1,	171: 1, H0644: 1,	H0169: 1, L0456: 1,	H0090: 1, H0264: 1,	412: 1, H0561: 1,	S0150: 1, S0002: 1,	H0529: 1, L0638: 1,	.0372: 1, L0649: 1,	.0388: 1, L0659: 1,	,0783: 1, L0789: 1,	.0791: 1, H0519: 1,	S0380: 1, H0522: 1,	H0436: 1, L0747: 1,	.0752: 1, L0757: 1,	.0599: 1, H0542: 1,	H0543: 1 and H0422: 1.		AR061: 0, AR089: 0	H0038: 3, H0156: 2,	L0455: 1, H0616: 1,	S0038: 1, H0538: 1 and S0028: 1
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Thr-144 to Ala-153,	Leu-214 to Pro-227,	Asp-245 to Arg-251,	Gly-261 to Gln-267,	Gly-283 to His-288,	Ser-326 to Gln-336,	Met-356 to Glu-361,	Ala-438 to Ile-444,	Ser-479 to Val-484,	Arg-490 to Arg-499,	Pro-509 to Gln-514,	Glu-622 to Ser-628,	Thr-653 to Arg-658,	Glu-678 to Asp-752.	•				•						Asn-25 to Trp-34,	Ile-51 to Asp-58,	Gln-87 to Pro-93.	
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.	AR089: 13, AR061: 8 S0152: 4, H0556: 3, H0265: 2, S3014: 2, H0543: 2, H0423: 2, H06402: 1, R0650: 1, H06402: 1, R0650: 1, H0659: 1, H0575: 1, H0618: 1, H0253: 1, H0618: 1, H0652: 1, S0182: 1, H0652: 1, H0651: 1, R0652: 1, H0651: 1, R0652: 1,		AR089: 39, AR061: 8 H0305: 3	
Asn-23 to Trp-32, Ile-49 to Asp-56, Gln-85 to Pro-91.	Ala-8 to Thr-23, Pro-35 to Met-41, Asn-60 to Thr-65, Asn-89 to Glu-94, Pro-161 to Leu-167, Asp-184 to Trp-189, Phe-192 to Leu-206, Arg-215 to Leu-221.	Ala-8 to Thr-23, Pro-35 to Met-41, Asn-60 to Thr-65, Asn-89 to Glu-94, Pro-161 to Leu-167, Asp-184 to Trp-189, Phe-192 to Pro-201, Pro-226 to Lys-231, Ala-237 to Pro-264.		Leu-43 to Tyr-48.
1794	1533	1795	1534	1796
3 - 809	3 - 668	3 - 818	319 - 77	1-177
894	633	895	634	968
908326	1220017	933546	1117318	908245
	HBUAC02		HCWEQ14 1117318	
	623	·	624	

AR089: 6, AR061: 2 S0252: 5, S0268: 5, S0256: 4, S0228: 3, S0270: 3, S0258: 2, H0305: 2, H0090: 2, H0521: 2, L0740: 2, L0777: 2, H0657: 1, S0212: 1, H0661: 1, H0580: 1, L0717: 1, H0438: 1, H0486: 1, T0074: 1, H0581: 1, S0388: 1, H0412: 1, L0637: 1, L0766: 1, L0791: 1, S0216: 1, L0755: 1, H0445: 1, L0755: 1, H0445: 1, L0755: 1, L0592: 1, L0581: 1, L0593: 1 and H0543: 1.		AR089: 63, AR061: 13 H0616: 3, H0521: 3, H0046: 2, H0038: 2, S0045: 1, H0550: 1, H0013: 1, S0386: 1, H0494: 1, S0150: 1, H0520: 1, H0436: 1 and L0595: 1.	
	Arg-68 to Ser-76.	Ser-3 to Arg-11, Gln-68 to Thr-77, Pro-194 to Lys-203.	Gln-49 to Thr-58, Pro-175 to Lys-184.
1535	1797	1536	1798
1 - 642	1 - 369	46 - 867	2 - 766
635	897	636	868
1228148	772569	1213567	908303
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625		626	

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113721, 247200, 600059, 601545																				
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AR089: 159, AR061: 142 H0486: 1	AR089: 3, AR061: 1 S0045: 1, S0050: 1, H0020: 1 and S0032: 1.		AR089: 2, AR061: 2	L0766: 2, L0665: 2, H0395: 1, S0212: 1,	S0360: 1, H0551: 1,	H0494: 1, L0639: 1,	L0521: 1, L0804: 1, H0682: 1 and L0749: 1.							AR089: 2, AR061: 1	T 0775. 5 T 0778. 7	101/0.0, 10/16.1,	LU/58: 4, LU622: 3,	H0599: 3, H0373: 3,	L0772: 3, L0777: 3,	L0757: 3, S0045: 2,
	Gly-114 to Gly-120, Pro-140 to Tyr-145, Asn-180 to Gly-185, Arg-274 to Ala-280, Gly-310 to Gly-317.	Gly-114 to Gly-120.	Pro-9 to Ala-19,	Ser-39 to Gly-46, Thr-54 to Glv-62.	Ile-77 to Arg-84,	Thr-122 to Met-132,	Gln-134 to Gln-147.	Pro-9 to Ala-19,	Ser-39 to Gly-46,	Thr-54 to Gly-62,	Ile-77 to Arg-84,	Thr-122 to Met-132,	Gin-134 to Gin-14/.	Ser-15 to Gln-23,	Gly-/9 to Asp-92,	GIY-105 to Cys-111.				
1537	1538	1799	1539					1800						1540						
162 - 371	2 - 967	2 - 409	1 - 642			÷		1-690						334 - 2						
637	638	668	639					900						640						
587710	1152485	973667	1107045		•			761293				_		1152487						
HDTDD72	HFRBN02		HKAIH72											HMAAD90 1152487						
627	628	_	629											630						

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L0021: 2, 80366: 2, 80144: 2, L0774: 2, L0541: 2, S0310: 2, L0604: 2, L0808: 1, S0116: 1, S0376: 1, S0360: 1, H0404: 1, L0623: 1, H0587: 1, L0623: 1, H0530: 1, H0622: 1, H0622: 1, H0622: 1, H0622: 1, H0622: 1, L0520: 1, L0521: 1, L0525: 1, L0525: 1, L0521: 1, L0525: 1, L0779: 1, L0777: 1, L0779: 1, L0772: 1, L0779: 1, L0752: 1, L0779: 1, L0752: 1, L0759: 1, L0752: 1, L0752: 1, L0759: 1, L0752: 1, L0752: 1, L0759: 1, L0752:	
<u> </u>	Asp-26 to Arg-32, Arg-74 to Leu-79, Ser-83 to Cys-95, Leu-108 to Thr-118, Gly-126 to Gly-131, Arg-162 to Pro-168,
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	AR089: 1, AR061: 0 S0144: 1 and H0521: 1.		AR061: 4, AR089: 1 S0152: 1 and L0601: 1.		AR061: 16, AR089: 6 H0617: 10, S0358: 5,	L0622: 4, H0620: 4,	H0658: 4, L0623: 3,	H0424: 3, H0549: 2,	H0550: 2, H0586: 2,	H0486: 2, H0546: 2,	L0769: 2, L0773: 2,	S0374: 2, S0206: 2,	L0743: 2, L0750: 2,	L0779: 2, L0731: 2,	L0601: 2, H0624: 1,	H0170: 1, H0171: 1,	H0686: 1, H0295: 1,	H0657: 1, H0484: 1,	H0255: 1, S0420: 1,
His-173 to Asp-178, Arg-196 to Ser-202, Arg-214 to Val-220, Ser-243 to Leu-253, Arg-275 to Ile-283, Lys-367 to Phe-374, Gln-384 to Gly-389,	Citt-450 to Eye-416.				His-91 to Gly-103, Glv-112 to Glv-117.	Glu-129 to Glu-136,													
	1541	1802	1542	1803	1543														
	3 - 374	189 - 497	82 - 405	82 - 408	154 - 783												-		
	641	902	642	903	643														
	1105540	729831	1105131	929723	1219545														
	HMABQ71 1105540		HPJEV95		HSKYR59														
	631		632		633														

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, S0360:	, H0455	, T0060	, H0599	, H0327	, H0545	, H0688	, H0213	, H0673	, \$0366:	, H0087	, H0334	, L0598:	, L0796:	, L0761:	, L0373:	, L0774:	, L0783:	, L0666:	, H0651:	, H0521:	, H0478:	, L0747:	, L0755:	.0757: 1, H0445: 1,	.0608: 1, L0361: 1	l, H0542: 1 and			4, ARO
S0376: 1, S0360: 1,	H0370: 1	H0587: 1, T0060: 1,	r0114: 1	H0122: 1	H0544: 1	H0188: 1	r0006: 1	H0606: 1, H0673: 1	S0364: 1, S0366: 1,	H0634: 1	H0413: 1, H0334: 1	30144: 1	.0763: 1	L0639: 1, L0761: 1,	.0772: 1	.0764: 1	L0775: 1, L0783: 1,	.0809: 1	L0663: 1, H0651:	30378: 1	S0392: 1, H0478: 1,	.0751: 1	.0752: 1	.0757: 1	.0608: 1	L0366: 1	H0543: 1		AR089: 4, AR061:
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50358: 5,	620: 4,	623: 3,	1549: 2,	586: 2,	546: 2,	773: 2,	206: 2,	750: 2,	731: 2,	624: 1,	171:1,	1295: 1,)484: 1,	420: 1,	360: 1,	0455: 1,	0060: 1,	599: 1,	0327: 1,	0545: 1,	0688: 1,	0213: 1,	0673:1,	366: 1,	0087:1,	0334: 1,	598: 1,)796: 1,	0761: 1,)373: 1,
H0617: 10, S0358: 5,	L0622: 4, H0620: 4,	H0658: 4, L0623: 3,	H0424: 3, H0549: 2,	H0550: 2, H0586: 2,	H0486: 2, H0546: 2,	L0769: 2, L0773: 2,	S0374: 2, S0206: 2,	L0743: 2, L0750: 2,	L0779: 2, L0731: 2,	L0601: 2, H0624: 1	H0170: 1, H0171:	H0686: 1, H0295:	H0657: 1, H0484:	H0255: 1, S0420: 1,	S0376: 1, S0360: 1,	H0370: 1, H0455: 1	H0587: 1, T0060:	T0114: 1, H0599:	H0122: 1, H0327: 1	H0544: 1, H0545: 1,	H0188: 1, H0688: 1	T0006: 1, H0213: 1,	H0606: 1, H0673:1	S0364: 1, S0366: 1	H0634: 1, H0087: 1	H0413: 1, H0334: 1,	S0144: 1, L0598:	L0763: 1, L0796:	L0639: 1, L0761: 1,	L0772: 1, L0373:
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L0764: 1, L0774: 1, L0775: 1, L0783: 1, L0809: 1, L0666: 1, L0663: 1, H0651: 1, S0378: 1, H0478: 1, L0751: 1, L0747: 1, L0752: 1, L0747: 1, L0752: 1, L0745: 1, L0757: 1, H0445: 1, L0608: 1, L0361: 1, L0366: 1, H0542: 1 and H0543: 1.		AR061: 6, AR089: 5	H0556: 8, H0617: 6,	L0659: 6, L0666: 6,	L0596: 6, H0441: 5,	L0665: 5, S0222: 4,	T0010: 4, S0038: 4,	H0657: 3, H0559: 3,	H0013: 3, H0494: 3,	L0804: 3, L0809: 3,	H0547: 3, S0152: 3,	H0521: 3, H0265: 2,	H0656: 2, L0717: 2,	S0278: 2, H0250: 2,	H0575: 2, S0049: 2,	H0620: 2, H0288: 2,	H0213: 2, S0036: 2,
	Ala-2 to Gly-15, Glu-120 to Ser-125.	Leu-14 to Ile-19,	Pro-69 to Pro-76,	Glu-86 to Thr-91,	Val-121 to Thr-127,												
	1805	1545															
	11 - 604	123 - 1442												•			
	905	645															
	933749	1164013					· · · · ·										
		HSXCW82					•										
		635	·														

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H0623: 2 L0766: 2 L0768: 2 S0028: 2 S0028: 2 H0422: 2 S0430: 1 H0637: 1 H0249: H0249: H0249: H0052: 2 R0346: 1 H0083: S0336: H0083: S0336: H0083: H0080: H00	T0041: T0041: N0647: S0002: 1 L0369: L0761: L0800:
H0634: 2, H0623: 2, L0764: 2, L0766: 2, L0775: 2, L0438: 2, H0682: 2, S0028: 2, H0682: 2, S0028: 2, H0224: 1, S0430: 1, L0785: 1, H0341: 1, S0212: 1, H0643: 1, H0580: 1, H0643: 1, H0089:	L0351: 1, T0041: 1, H0429: 1, H0647: 1, S0210: 1, S0002: 1, H0529: 1, L0369: 1, L0769: 1, L0761: 1, L0372: 1, L0800: 1,
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		103050, 103050,	124030,	124030,	182380,	188826,	190040,	190040, 190040			
·		22q13.1-q13.2 103050, 103050,									
L0794: 1, L0803: 1, L0806: 1, L0509: 1, L0657: 1, L0383: 1, L0787: 1, L0663: 1, S0374: 1, H0523: 1, H0658: 1, H0522: 1, H0134: 1, H0555: 1, L0612: 1, S3012: 1, S0037: 1, S3014: 1, S0037: 1, L0439: 1, L0749: 1, L0752: 1, S0031: 1, L0592: 1, H0667: 1, S0276: 1,			L0748: 3, H0265: 2,	H0556: 2, H0551: 2, H0494: 2, 1,0770: 2.	L0758: 2, L0599: 2,	L0361: 2, H0650: 1,	H0657: 1, H0381: 1,	H0419: 1, H0427: 1, H0618: 1, H0421: 1	H0530: 1, H0546: 1,	H0413: 1, H0625: 1,	L0369: 1, L0644: 1, L0521: 1, L0375: 1,
	Leu-14 to Ile-19.	Arg-1 to Thr-11, Pro-23 to Met-29,	Asn-48 to Thr-53,	Asn-77 to Glu-82, Pro-149 to I en-155	٠. ٠		Arg-203 to Leu-209.				
	1806	1546							-		
	115 - 387	2 - 631									
	906	646									
	739372	933545									
		HSYDB42									
		989									

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L0783: 1, L0809: 1, L0789: 1, H0144: 1, S0374: 1, L0565: 1, H0658: 1, S0330: 1, H0539: 1, L0777: 1, L0731: 1, H0542: 1 and H0506: 1.	AR089: 3, AR061: 3 L0748: 9, S0356: 8, S0358: 8, L0471: 5, H0144: 5, L0740: 5, H0556: 3, S0354: 3, H0556: 3, S0354: 3, H0083: 3, T0042: 3, H0083: 3, T0042: 3, H0083: 3, T0042: 3, H0083: 2, H0043: 3, H0083: 2, H0013: 2, H0086: 2, H0013: 2, H0086: 2, H0013: 2, H0086: 2, H0013: 2, H0086: 2, H0561: 2, H0086: 2, H0561: 2, H0012: 1, H0583: 1, H0159: 1, H0583: 1, H0159: 1, H0583: 1, H0155: 1, S0418: 1, S0212: 1, R0418: 1,
	Pro-3 to Leu-9, Glu-12 to Val-22, Gln-27 to Glu-33, Pro-68 to Glu-75.
	1547
	2 - 421
	647
	1193059
	HTXKJ79
	637

S0045: 1, H0411: 1, H0369: 1, H0586: 1, H0497: 1, H0643: 1, H00331: 1, S0010: 1, H0052: 1, H0327: 1, H0054: 1, H0012: 1, H0011: 1, H0012: 1, H0014: 1, H0015: 1, H0039: 1, H0266: 1, H0688: 1, H0124: 1, H0135: 1, H0640: 1, H0529: 1, H0691: 1, H0547: 1, H0519: 1, H0547: 1, H0519: 1, H0521: 1, S0037: 1, S0328: 1, H0518: 1, H0521: 1, S0037: 1, S0328: 1, H0518: 1, H0521: 1, S0028: 1, L0742: 1, L0752: 1, L0755: 1, S0026: 1,	•	AR089: 2, AR061: 2 S0252: 5, S0268: 5, S0256: 4, S0228: 3, S0270: 3, S0258: 2, H0305: 2, H0090: 2, H0521: 2, L0740: 2, L0777: 2, H0657: 1,
		Gly-1 to Val-6, Ser-31 to Asn-41, Ser-61 to Lys-66, Lys-99 to Asn-105, Glu-190 to Thr-197.
	1807	1548
	99 - 443	556 - 1251
	206	648
	938963	1165320
·		HUSGQ19
		638

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										•						
S0212: 1, H0661: 1, H0580: 1, L0717: 1, H0438: 1, H0486: 1, T0074: 1, H0581: 1, S0388: 1, H0412: 1, L0637: 1, L0766: 1, L0791: 1, S0216: 1, H0670: 1, S0380: 1, L0755: 1, H0445: 1, L0605: 1, L0592: 1, L0581: 1, L0593: 1 and H0543: 1.		AR089: 1, AR061: 1	L0769: 10, L0754: 10,	L0766: 5, L0803: 4,	L0756: 4, L0779: 4,	L0780: 4, L0748: 3,	L0753: 3, H0620: 2,	H0264: 2, L0770: 2,	L0806: 2, L0741: 2,	L0747: 2, L0604: 2,	H0265: 1, H0556: 1,	H0657: 1, H0656: 1,	H0341: 1, H0392: 1,	H0331: 1, H0559: 1,	H0427: 1, L0021: 1,	H0173: 1, H0052: 1,
,	Arg-1 to Asp-13, Arg-81 to Ser-89, Gly-128 to Gly-143.	Arg-54 to Pro-67,	Arg-82 to Ala-90,	Gln-105 to Asp-115.	•											
	1808	1549														
	2 - 517	1 - 519														
	806	649														
	772568	1193982												·		
		HUSZS75														
		639														

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				_,					
			,						
T0115: 1, H0188: 1, H0135: 1, H0413: 1, H0561: 1, H0647: 1, L0763: 1, L0761: 1, L0774: 1, L0651: 1, L0776: 1, L0659: 1, L0776: 1, L0787: 1, L0791: 1, L0792: 1, H0684: 1, H0521: 1, L0777: 1, L0752: 1,		AR089: 5, AR061: 1 H0551: 2, S0420: 1,	H0580: 1, H0586: 1,	H0521: 1.				AR061: 5, AR089: 4 L0771: 12, H0040: 2,	H0539: 2, H0306: 1, H0617: 1 and H0135: 1.
	Arg-7 to Thr-13.	5,	~~		Asp-172 to Asp-180,	Lys-247 to Asn-252, Glv-336 to Tm-342	Lys-37 to Asn-42, Glv-126 to Trp-132.		
	1809 A	1550 Pr	<u> </u>	₹ ₹	<u>A</u>	<u>17. G</u>	1810 L	1551	
·	18	15					188	151	
	64 - 918	3 - 1259					3 - 542	341 - 3	
	606	650					910	651	
	908443						659873	954855	
		HWBDR25						HBGSS51	
·		640						641	

[42] The first column in Table 1A provides the gene number in the application corresponding to the clone identifier. The second column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

- [43] The third column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The fourth column provides the "SEQ ID NO:" identifier for each of the contig polynucleotide sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 6, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.
- [44] The sixth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 5. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.
- [45] Column 7 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A.

It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

[46] Column 8 in Table 1A provides an expression profile and library code: count for each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression.

[47] Column 9 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is

assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[48] A modified version of the computer program BLASTN (Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the 'Query'). A sequence from the UniGene database (the 'Subject') was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIMTM (supra). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 10, Table 1A, labelled "OMIM Disease Reference(s)". Table 5 is a key to the OMIM reference identification numbers (column 1), and provides a description of the associated disease in Column 2.

TABLE 1B

Clone ID	SEQ ID	CONTIG	BAC ID: A	SEQ ID	EXON
NO:Z	NO:X	ID:		NO:B	From-To
HADTU18	26	666268	AC067849	1811	1-1270
HADTU18	26	666268	AC067849	1812	1-408
HYAAH23	42	1032585	AL158156	1813	1-134
					381-1154
					1539-2051
				l N	2660-4011
					4082-4116
				1	4578-5063
					5736-6373
ŀ					6388-6981
					7052-7364
		İ			7527-7659
į					7698-7943
					9535-9659
				,	9671-10133
					11759-12221
HYAAH23	42	1032585	AL158155	1814	1-171
					2177-2317
	-				2558-3332
				·	3786-4298
					4772-6123
	į				6194-6228
-			l		6690-7175
		ĺ			7848-8485
					8500-9065
	İ				9164-9476
					9639-9771
		ŕ			9810-10055
ı					11647-11771
·					11783-12245
					13870-14332
HYAAH23	42	1032585	AL158156	1815	1-4481
HYAAH23	42	1032585	AL158155	1816	1-4477
HAJAV28	45	948630	AL121579	1817	1-175
					1520-1889
					2329-2473
-					2730-2805
					3231-3444
					4096-4273
					7815-7900
				!	8874-9058
HCE1S21	49	671209	AC007666	1818	1-122
			·		274-371

					3724-3890
					4511-4668
		ĺ		Į	5669-6372
177071001					6679-7654
HCE1S21	49	671209	AC000052	1819	1-122
	İ				274-371
}	-				1127-1238
					3724-3890
					4511-4668
	1				5669-6372
					6679-7654
HCE1S21	49	671209	AC004019	1820	1-122
	ļ				274-371
1	}				1127-1238
	1			ļ	3724-3890
	ŀ				4511-4668
:					5669-6372
					6679-7654
HCE1S21	49	671209	AC007666	1821	1-269
					324-413
HCE1S21	49	671209	AC007666	1822	1-591
					2367-2471
Į					4522-4940
					4990-5100
					6036-6133
				1	6225-6754
Į.	[•		7871-7959
					8764-9481
HCE1S21	49	671209	AC000052	1823	1-269
					324-413
HCE1S21	49	671209	AC000052	1824	1-591
					2366-2473
HCE1S21	49	671209	AC004019	1825	1-269
					324-413
HCE1S21	49	671209	AC004019	1826	1-462
HCE3J64	50	951228	AC061705	1827	1-77
					614-729
				1	917-1028
					1154-1218
		ļ			1398-1591
					1704-1802
					2419-3315
HCFLI54	52	921382	AC023278	1828	1-1977
					2006-3504
					3802-4090
					4113-6041
					6143-6242
					6252-6919

					7-2
1					6933-7614
TIOPLICA	-50	-	1.0005555	1.5.5.	7682-8351
HCFLI54	52	921382	AC005562	1829	1-3490
		[3783-4087
					4094-6238
		Į			6249-6901
					6930-7364
TIODI TO A	+50				7701-8350
HCFLI54	52	921382	AC023278	1830	1-574
YIOTY YOU	+	001000			774-1443
HCFLI54	52	921382	AC023278	1831	1-616
HCFLI54	52	921382	AC005562	1832	1-667
HCWDL45	55	889416	AC023100	1833	1-1181
HCWDL45	55	889416	Z98747	1834	1-1181
HDPGQ74	59	691163	AC073462	1835	1-173
					1923-2056
		1			2270-2362
	İ			1	4504-5101
			·		5444-5630
					6218-6268
	}				8466-8542
	1				8816-8888
					10396-10437
HDPGS68	60	752975	AC034180	1836	1-950
HE2FR50	64	508498	AC010408	1837	1-574
	į ·			ļ	1043-1729
	` †	{			1759-1995
					2866-3391
	}	1			3406-3626
					3954-4396
		· ·		1	4444-4667
]				5413-5515
	ŀ				8692-8774
	Ì]			8878-9828
					13011-13373
					14082-14365
HEDGER		0.60.650			15285-16319
HEBGK01	67	963673	Z97653	1838	1-627
					815-1256
TIPP CITAL				ļ	2165-2714
HEBGK01	67	963673	Z97653	1839	1-146
HEBGK01	67	963673	Z97653	1840	1-487
HEFMB30	68	691516	AC016659	1841	1-862
HEFMB30	68	691516	AC012481	1842	1-862
HEFMB30	68	691516	AC016659	1843	1-447
HEFMB30	68	691516	AC012481	1844	1-447
HEOPE58	69	851009	AL078634	1845	1-40
	<u> </u>			<u> </u>	1089-1226

					
	Ì			ļ	3206-3637
				İ	4312-4463
					7455-8330
				}	8603-8815
					9078-9190
1 .			1	-	9522-9767
					10946-12260
					13754-14357
1	+				15092-15830
					18660-18822
				1	21128-21635
		ļ			21685-21721
HEOPE58	69	851009	AL078634	1846	1-235
					3051-3154
•		-			3199-3734
HEOPE58	69	851009	AL078634	1847	1-444
HLHDD45	75	942901	AC024148	1848	1-116
			110024140	1040	629-787
· ·	1				1238-1305
					1825-1969
-					2522-2966
					l l
HLHDD45	75	942901	AC069253	1849	2984-6238
TIBLES 15	'3	342301	AC009233	1849	1-116
	1.				629-787
l	1				1238-1305
·					1824-1968
					2521-2965
HLHDD45	75	0.40004			2983-5879
HLHDD45	/3	942901	AC044892	1850	1-116
	j				629-787
			· '	1	1238-1305
			1		1824-1968
		1		ļ	2521-2965
					2983-6236
HLHDD45	75	942901	AC044892	1851	1-105
HLHDD45	75	942901	AC069253	1852	1-105
HNHEQ86	79	785580	AC024653	1853	1-731
HSICX21	88	531267	AC016333	1854	1-552
HSICX21	88	531267	AC024101	1855	1-551
HSICX21	88	531267	AC016333	1856	1-448
HSICX21	88	531267	AC024101	1857	1-447
HSODC08	91	966264	AC005332	1858	1-1096
		7 0020-1	110003332	1030	
					1112-1196
		}			2142-2580
					2893-3071
			1		3148-3485
					4737-5087
	L			1	6182-6336

<u></u>	T		T	Ţ	6503-6667
					7642-8422
					8767-9265
HSODC08	91	966264	AC005332	1859	1-205
INDODCOO		300204	AC003332	1655	221-693
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HMICO24	406	677036	AC010925	2115	1-156
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				İ	10231-10522
	}				11163-11210

[50] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

ABLE 2

Clone ID	Contig	SEQ	Analysis	PFam/NR Description	PFam/NR Accession	Score/	IN	NT
NO:Z	ä	a	Method		Number	Percent	From	To
		NO:X				Identity		
HHMMC14	1152250	11	blastx.2	GLYOXYLATE	galgourd/loaned	%96	501	1088
				REDUCTASE (EC	7			
				1.1.1.79).				
HHMMC14	969371	652	HMMER	PFAM: D-isomer specific	PF00389	217.83	336	965
			1.8	2-hydroxyacid				
				dehydrogenases				
			blastx.14	(AF146018)	gi 5639830 gb AAD4	%96	<i>L</i> 8	1070
				hydroxypyruvate	5886.1 AF146018_1			
				reductase [Homo sapiens]	:			
HSLEQ79	1184946	12	blastx.2	D-lactate dehydrogenase	pir G64888 G64888	93%	674	156
				(EC 1.1.1.28) -				
				Escherichia coli				
HSLEQ79	752382	653	HMMER	PFAM: D-isomer specific	PF00389	222	19	453
			2.1.1	2-hydroxyacid				
				dehydrogenases				
HUCME08	1082023	13	blastx.2	GLYOXYLATE	paneo/109ubq	%88	110	625
				REDUCTASE (EC	7	100%	54	107
				1.1.1.79).				
HUCME08	08/898	654	HMMER	PFAM: D-isomer specific	PF00389	93.4	275	556
	· - .		2.1.1	2-hydroxyacid				
				dehydrogenases				
HNGOW33	1152254	14	blastx.2	8-amino-7-oxononanoate	pirlD32025 SYECKP	%16	547	1158
				synthase (EC 2.3.1.47) -		%02	336	497
				Escherichia coli				

HNG0W33	957351	655	HIMMER	PFAM:	PF00222	441.9	409	1251
			2.1.1	Aminotransferases class-II				
	•		blastx.14	(AE000195) orf,	gi 1787167 gb AAC7	%66	2714	3712
				hypothetical protein	4022.1		-	
				Escherichia coli]				
HT4GD03	1103896	15	blastx.2	2-AMINO-3-	sp 075600 KBL_HU	93%	153	896
				KETOBUTYRATE	MAN	100%	89	166
				COENZYME A LIGASE,				
				MITOCHONDRIAL 1			-	
HT4GD03	923731	959	HMMER	PFAM:	PF00222	78.93	575	877
			1.8	Aminotransferases class-II				
			blastx.14	dJ466N1.2 (2-amino-3-	gi 4808241 emb CAB	100%	584	196
				ketobutyrate-CoA ligase	42830.1	87%	153	569
				mRNA, 1		100%	140	166
HAQBZ89	949061	16	HMMER	PFAM:	PF00202	62.49	89	325
			1.8	Aminotransferases class-				
				III pyridoxal-phosphate				
			blastx.2	CG8745 PROTEIN.	sp Q9VU95 Q9VU95	52%	∞	316
HCCCC81	949062	17	HMMER	PFAM:	PF00202	178.37	187	816
			1.8	Aminotransferases class-				
				III pyridoxal-phosphate				
			blastx.2	hypothetical protein	pir T25848 T25848	46%	190	879
				T01B11.2 -			•	
				Caenorhabditis elegans				
HE8PW83	927532	18	HMMER	PFAM:	PF00202	139.27	4	465
			1.8	Aminotransferases class-				
				III pyridoxal-phosphate				
			blastx.2	ALANINE	sp Q64565 AGT2_R	83%	4	546
				GLYOXYLATE	AT	!	,	
_				AMINOTRANSFERASE				

	-			2 PRECTIPACION (FC 1 1				
TTTOOOTT	000000	5	470 041	PENSON EO L	000000			
HE9QQ22	949080	61	HMMEK	PFAM:	PF00202	105.1	285	545
			2.1.1	Aminotransferases class-				
		٠		III pyridoxal-phosphate				
			blastx.2	ALANINE	sp Q64565 AGT2 R	51%	3	1070
			_	GLYOXYLATE	AT	43%	545	1003
				AMINOTRANSFERASE		46%	682	666
				2 PRECURSOR (EC 1 1				
HFPFB39	946170	20	HMMER	PFAM:	PF00202	235.05	1613	714
			1.8	Aminotransferases class-				
				III pyridoxal-phosphate				
			blastx.2	hypothetical protein	pirT25848 T25848	49%	1613	651
				T01B11.2 -				
				Caenorhabditis elegans				
HSDJI44	1151680	21	blastx.2	adenosylmethionine8-	pir/F64813/XNECDP	%96	857	2143
•••				amino-7-oxononanoate			•	-
				transaminase (EC		•		
				2.6.1.62) - Escherichia				_
				coli		*		
HSDJI44	974784	657	HMMER	PFAM:	PF00202	511.4	894	1835
			2.1.1	Aminotransferases class-				
				III pyridoxal-phosphate				
		_	blastx.14	(AE000180) 7,8-	gi 1786991 gb AAC7	%66	795	1841
				diaminopelargonic acid	3861.1	100%	1837	1860
				synthetase [Escherichia			•	
				coli]				-
HE9DG38	1181748	22	blastx.2	Putative selenocysteine	sp AAF36816 AAF36	%66	44	994
	_			lyase.	816			
HE9DG38	943384	859	HIMMER	PFAM:	PF00266	215.1	160	1326
			2.1.1	Aminotransferases class-				_
-	-	-						

HGBAT24 1024746 23 blastx.2 phosphoserine pir Bg4830 B64830 (Caenorhabditis elegans) (Λ				
Caenorhabditis elegans 1024746				blastx.14	similar to NIFS protein	gi 722379 gb AAC46	45%	442	678
1024746 23 blastx.2 phosphoserine transaminase (EC 2.6.1.52) - Escherichia coli 761143 659 HMMER PFAM: 1181747 24 blastx.2 CDNA FLJ10515 FIS, CLONE NT2RP2000764, WEAKLY SIMILAR TO 1 NTMER PFAM: 2.1.1 Aminotransferases class-V blastx.2 (AF175767) putative selencysteine lyase [HMMER PFAM: Cytochrome C 1.8 and Quinol oxidase Polypeptide I blastx.2 cytochrome-c oxidase (EC 1931) chain I - human		T			(muogen manon) [Caenorhahditis elegans]	1,000	61%	724	840
1024746 23 blastx.2 phosphoserine transaminase (BC 2.6.1.52) - Escherichia coli 761143 659 HMMER PFAM: 1181747 24 blastx.2 CDNA FLJ10515 FIS, WEAKLY SIMILAR TO 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	· • ·						46%	1210	1344
1024746 23 blastx.2 phosphoserine transaminase (EC 2.6.1.52) - Escherichia coli 761143 659 HMMER PFAM: 2.1.1 Aminotransferases class- V I181747 24 blastx.2 CDNA FLJ10515 FIS, CLONE NT2RP2000764, WEAKLY SIMILAR TO 1 Aminotransferases class- V blastx.2 (AF175767) putative selenocysteine lyase HMMER PFAM: C68405 25 HMMER PFAM: Cytochrome C 1.8 and Quinol oxidase blastx.2 cytochrome-c oxidase (EC 19.3.1) Chain 1 - human							41%	1081	1209
1024746 23 blastx.2 phosphoserine transaminase (EC 2.6.1.52) - Escherichia coli (2.1.1 Aminotransferases class-1.1.1 Aminotran							57%	313	375
1024746 23 blastx.2 phosphoserine transaminase (EC 2.6.1.52) - Escherichia coli Coli Aminotransferases class-2.1.1 Aminotransferases class-1181747 24 blastx.2 CDNA FLJ10515 FIS, WEAKLY SIMILAR TO 1 1 Aminotransferases class-2.1.1 Aminotransferases class-2.1.1 Aminotransferases class-2.1.1 Aminotransferases class-2.1.1 Aminotransferases class-3.1.1 Aminotransferase							41%	1379	1450
transaminase (EC 2.6.1.52) - Escherichia coli 761143 659 HMMER PFAM: V Aminotransferases class- V CLONA FLJ10515 FIS, CLONE NT2RP2000764, WEAKLY SIMILAR TO 1 N Aminotransferases class- 12.1.1 Aminotransferases class- N blastx.2 (AF175767) putative selencysteine lyase [Homo 1 C68405 25 HMMER PFAM: Cytochrome C HMMER PFAM: Cytochrome C Homo 1 Dolypeptide I Dolypeptide I Diastx.2 cytochrome-c oxidase (EC	HGBAT24	1024746	23	blastx.2	phosphoserine	pir B64830 B64830	%16	1	369
2.0.1.32) - Eschercula coli 761143 659 HMMER PFAM: 2.1.1 Aminotransferases class- V I181747 24 blastx.2 CDNA FLJ10515 FIS, CLONE NT2RP2000764, WEAKLY SIMILAR TO 1 Aminotransferases class- 2.1.1 Aminotransferases class- blastx.2 (AF175767) putative selenocysteine lyase [Homo 1] Romo 1 HMMER PFAM: Cytochrome C 1.8 and Quinol oxidase blastx.2 cytochrome-c oxidase (EC 19.3.1) chain 1 - human					transaminase (EC				
761143 659 HMMER PFAM: 2.1.1 Aminotransferases class- v 1181747 24 blastx.2 CDNA FLJ10515 FIS, CLONE NT2RP2000764, WEAKLY SIMILAR TO 1 1 Aminotransferases class- 2.1.1 Aminotransferases class- blastx.2 (AF175767) putative selenocysteine lyase [Homo 1] 668405 25 HMMER PFAM: Cytochrome C 1.8 and Quinol oxidase blastx.2 cytochrome-c oxidase (EC 193.1) chain 1 - human					coli				
2.1.1 Aminotransferases class- V 1181747 24 blastx.2 CDNA FLJ10515 FIS, CLONE NT2RP2000764, WEAKLY SIMILAR TO 1 1 Aminotransferases class- 2.1.1 Aminotransferases class- blastx.2 (AF175767) putative selenccysteine lyase [Homo 1] Homo 1 Homo	HGBAT24	761143	659	HMMER	PFAM:	PF00266	128.3	10	369
1181747				2.1.1	Aminotransferases class-				
1181747 24 blastx.2 CDNA FLJ10515 FIS, CLONE NT2RP2000764, WEAKLY SIMILAR TO 1 1 Aminotransferases class- 2.1.1 V blastx.2 (AF175767) putative selenocysteine lyase [Homo 1] 668405 25 HMMER PFAM: Cytochrome C 1.8 and Quinol oxidase polypeptide I blastx.2 cytochrome-c oxidase (EC 1 blastx.2 cytochrome-c oxidase (EC					\				
CLONE N12RP2000764, WEAKLY SIMILAR TO 1	HTDAF92	1181747	24	blastx.2	CDNA FLJ10515 FIS,	spBAA91659BAA9	100%	256	1011
WEAKLY SIMILAR TO 1 1 1 1 1 1 1 1 1					CLONE NT2RP2000764,	1659			
943385 660 HMMER PFAM: 2.1.1 Aminotransferases class- V blastx.2 (AF175767) putative selenocysteine lyase [Homo 1 FAM: Cytochrome C 1.8 and Quinol oxidase polypeptide I blastx.2 cytochrome-c oxidase (EC 1 93.1) chain 1 - human					WEAKLY SIMILAR TO				
2.1.1 Aminotransferases class- V V blastx.2 (AF175767) putative selenocysteine lyase [Homo 1 Homo 1 668405 25 HMMER PFAM: Cytochrome C 1.8 and Quinol oxidase polypeptide I blastx.2 cytochrome-c oxidase (EC 1.9 3.1) chain 1 - human	HTD A FO7	043385	999	HWMFR	PFAM.	PF00266	104.6	163	597
blastx.2 (AF175767) putative selenocysteine lyase [Homo 1 Homo 1 1.8 and Quinol oxidase polypeptide I blastx.2 cytochrome-c oxidase (EC 1931) chain I - human	7/11/11/11))	2.1.1	Aminotransferases class-				
blastx.2 (AF175767) putative selenocysteine lyase [Homo 1 Homo 1 1.8 PFAM: Cytochrome C 1.8 and Quinol oxidase polypeptide I blastx.2 cytochrome-c oxidase (EC 19 3.1) chain 1 - human					Λ				
selenocysteine lyasc [Homo 1 668405 25 HIMMER PFAM: Cytochrome C 1.8 and Quinol oxidase polypeptide I blastx.2 cytochrome-c oxidase (EC 1 9 3 1) chain 1 - human				blastx.2	(AF175767) putative	gb AAF36816.1 AF1	100%	160	627
668405 25 HMMER PFAM: Cytochrome C 1.8 and Quinol oxidase polypeptide I blastx.2 cytochrome-c oxidase (EC					selenocysteine lyase	75767_1			
668405 25 HMMER PFAM: Cytochrome C 1.8 and Quinol oxidase polypeptide I blastx.2 cytochrome-c oxidase (EC 1 9 3 1) chain I - human					[Homo 1				
and Quinol oxidase polypeptide I cytochrome-c oxidase (EC	HAPSI19	668405	25	HIMMER	PFAM: Cytochrome C	PF00115	75.81	263	382
polypeptide I cytochrome-c oxidase (EC				1.8	and Quinol oxidase				
cytochrome-c oxidase (EC 1931) chain I - human					polypeptide I				
1 0 3 1) chain 1 - himan				blastx.2	cytochrome-c oxidase (EC	pir A00463 ODHU1	76%	<u>س</u> ;	263
LICIOLA) CARACTER ASSESSED		_			1.9.3.1) chain I - human		%56	263	382

								_													- 1					-	
87	399	307	436			887	1714	1 / 14	905	1749	506	512	75		1339		1297		1324			1350		1371			565
28	385	185	2			369	921	170	279	1705	75	78	4		164		467		149			643		619			146
20%	100%	8.66	48%			102.61	400/	47%	45%	%09	159.13	46%	44%		%56		248.4		%68			196.9		38%			202.9
		PF00116	pir A00472 OBHU2			PF00067	02000 4 12 1 0000 1	pir(532313)A29368			PF00067	sp Q9VA27 Q9VA27			sp Q9Z1Z6 Q9Z1Z6		PF00481		gi 3777604 gb AAC9	7497.1		PF00481		pir T50783 T50783			PF00282
mitochondrion		PFAM: Cytochrome C oxidase subunit II	cytochrome-c oxidase (EC	1.9.3.1) chain II - human	mitochondrion	PFAM: Cytochrome P450		prostaglandin omega-	hydroxylase (EC 1.14.15) cytochrome 1	PFAM: Cytochrome P450	CYTOCHROME P450	4C3 (EC 1.14.14.1)	(CYPIVC3).	PROTEIN	PHOSPHATASE 2C.	PFAM: Protein	phosphatase 2C	(AF095927) protein	phosphatase 2C [Rattus	norvegicus]	PFAM: Protein	phosphatase 2C	protein phosphatase 2C-	like protein - Arabidopsis	thaliana	PFAM: Pyridoxal-
		HMMER 1.8	blastx.2			HIMMER	1.0	blastx.2			HMMER 1.8	blastx.2			blastx.2		HMMER	2.1.1	blastx.14			HMMER	2.1.1	blastx.2			HMMER
		26				27					28				29		662					30					31
		666268				954852					954849				1193068		918014		-			933635					926930
		HADTU18				HNTEF53					HWLLB11				HCRQK86		HCRQK86					HOCOT88					HELEF11

			2.1.1	dependent decarboxylase				
				conserved domain				
			blastx.2	glutamate decarboxylase	pir/B43332 B43332	81%	131	721
				(EC 4.1.1.15) beta -		100%	45	152
				Escherichia coli		999	595	780
						47%	564	620
HOUGD29	1204714	32	blastx.2	PANCREAS-ENRICHED	VHU90/EVHU90/qs	%26	202	1821
)				PHOSPHOLIPASE C.	3	79%	3	203
HOUGD29	767606	663	HMMER	PFAM:	PF00387	118.2	202	453
			2.1.1	Phosphatidylinositol-		•		
				specific phospholipase C,				
				Y domain				
			blastx.14	(AF044576)	gi[2957270]gb AAC3	42%	202	753
				phospholipase C PLC210	8963.1	35%	757	873
				[Caenorhabditis elegans]		28%	168	203
HSIGN57	910078	33	HMMER	PFAM:	PF00387	159.3	131	484
			2.1.1	Phosphatidylinositol-			_	-
				specific phospholipase C,				
				Y domain				
			blastx.2	PHOSPHOLIPASE C-L2.	sp Q9QYG1 Q9QYG	83%	7	754
HTFPF35	948475	34	HMMER	PFAM:	PF00387	163.8	839	507
) : : : :		2.1.1	Phosphatidylinositol-				-
				specific phospholipase C,				
				Y domain				
	•		blastx.2	1-phosphatidylinositol-	pir S14113 S14113	48%	839	06
				4,5-bisphosphate				
				phosphodiesterase 1				
HUFDB74	1227205	35	blastx.2	PHOSPHOINOSITIDE-	sp Q91423 Q91423	%09	7	547
				or non-				

	127	581	1081	1081	1462	429	447	565 759	209	629
	2	54	2286	2370	770	55	452	188 574	275	188
·	89.4	%86	663.4	95%	54%	37.62	58% 43%	57% 59%	37.58	52%
	PF00387	pir JC2347 JC2347	PF00155	gil79104 gb AAA35 568.1	sp Q9W698 Q9W698	PF00155	gi 4426837 gb AAD2 0564.1	sp Q9W698 Q9W698	PF00155	ph/AAD20564.11
PHOSPHOLIPASE C (FRAGMENT).	PFAM: Phosphatidylinositol- specific phospholipase C, Y domain	growth/differentiation factor 5 - human	PFAM: Aminotransferases class-I	aspartate aminotransferase precursor (2.6.1.1) [Homo sapiens]	1- AMINOCYCLOPROPAN E-CARBOXILATE SYNTHASE.	PFAM: Aminotransferases class-I	(AF108420) 1- aminocyclopropane- carboxilate synthase [Fugu rubripes]	1- AMINOCYCLOPROPAN E-CARBOXILATE SYNTHASE.	PFAM: Aminotransferases class-I	(AF108420) 1-
	HMMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.14	blastx.2	HMMER 1.8	blastx.14	blastx.2	HMMER 1.8	blastx 2
	664	36	599		37	999		38	299	
	901451	1229908	957228		1198479	944629		.1150836	936688	
	HUFDB74	HBXAB33	HBXAB33		HMABF84	HMABF84		HPTVF17	HPTVF17	

				aminocyclopropane-				
				carboxilate synthase				
				[Fugu rubripes]				
	1197407	39	blastx.2	aspartate transaminase	pir A00598 XNECD	%96	115	345
				(EC 2.0.1.1) - Escuencina coli				
	506582	899	HMMER	PFAM:	PF00155	97.17	106	363
			1.8	Aminotransferases class-I				
	1228138	40	blastx.2	aspartate transaminase	pir A00598 XNECD	%86	2	226.
		·		(EC 2.6.1.1) - Escherichia				
			4.0	COM	prootes	105.1	,	271
	0/.5959	600	HMMEK 2.1.1	PFAM: Aminotransferases class-I	FFUULOS	133.1	n	3/1
HTXSM05	1104951	41	blastx.2	alanine transaminase (EC	pir A40465 A40465	%19	5	406
				2.6.1.2), cytosolic -		%02	456	515
				human				
HTXSM05	958447	029	HMMER	PFAM:	PF00155	38.39	23	316
			1.8	Aminotransferases class-I				
			blastx.14	alanine aminotransferase	gi[1507680 dbj]BAA0	%99	5	358
				[Homo sapiens]	1186.1			
HYAAH23	1032585	42	blastx.2	GLYOXYLATE	9090BQ7 Q90BQ	95%		909
_				REDUCTASE (EC	7			
HTPDX13	1134372	43	blastx.2	CARBOXYPEPTIDASE	sp O54860 O54860	%88	2	922
				X2.				
HTPDX13	948419	671	HMMER	PFAM: Zinc	PF00246	87.75	257	682
			1.8	carboxypeptidases				
			blastx.14	(AF017639)	gi[2921092 gb AAC0	%88	2	922
				carboxypeptidase X2	4670.1			
				[Mus musculus]				

1981	1927	1974	2273	2355	1889	2452	322	230	458		146	347	101	88	210	124	292		563	599
2538		2186		2510		2541	275	120	96		102	3	09	89	163	41	224		234	3
41%	38%	48%	40%	38%	26%	41%	4.22	35.9	%26		6.42	40%	3.63	3.61	4.17	%09	43%		154.1	94%
sp O60448 O60448	-						PF00099	PF00022	sp AAF67655 AAF67	655	PF00099	sp Q9VKB2 Q9VKB	PF00099	PF00099	PF00099	pir/T29225/T29225			PF01431	sp O60344 ECE2_HU
NEURONAL THREAD	PROTEIN AD7C-NTP.						PFAM: Zinc-binding metalloprotease domain	PFAM: Actin	Uncharacterized	hypothalamus protein HARP11.	PFAM: Zinc-binding metalloprotease domain	CG5336 PROTEIN.	PFAM: Zinc-binding metalloprotease domain	PFAM: Zinc-binding	PFAM: Zinc-binding	hypothetical profein	F55G1.5 - Caenorhabditis	elegans	PFAM: Peptidase family	ENDOTHELIN-
blastx.2							HMMER 18	HMMER 2.1.1	blastx.2		HMMER 18	blastx.2	HIMMER 1.8	HMMER 1.8	HMMER	hlasty 2	7:47:57		HMMER	blastx.2
44	:						672	45			46		673	674	49		. —		50	
1172244							06830	948630			712955		772797	557243	671209				951228	
HAHHE43	Charmer						HAHHE43	HAJAV28			HAPOR59		HBIBF78	HCDAJ15	HCE1821				HCE3164	

889		571	100	50c	1124	1134		001	201	1	133	9	108	1	430			3	273	,	01				2921	1808	2108	2744
557		542	124	704	101	101		200	834	,	98		171		215				226		300				2613	1482	2049	2637
%65		3.55		0.41	2000	78%			5.29		5.78		4.63		93%				9.8		75%	_			%19	52%	100%	38%
MAN		PF00099		PF00099		pir(T29006/T29006			PF00099		PF00099		PF00099		pir S57525 S57525		-		PF00099		gi[887431 emb CAA5	2057.1			sp 060585 060585			
CONVERTING	ENZYME 2 (EC	PFAM: Zinc-binding	metalloprotease domain	PFAM: Zinc-binding	metalloprotease domain	hypothetical protein	ZK328.4 - Caenorhabditis	elegans	PFAM: Zinc-binding	metalloprotease domain	PFAM: Zinc-binding	metalloprotease domain	PFAM: Zinc-binding	metalloprotease domain	alcohol dehydrogenase	(EC 1.1.1.1) C-	Escherichia coli (isolate	VU 3685)	PFAM: Zinc-binding	metalloprotease domain	formaldehyde	dehydrogenase	(glutathione) [Escherichia	colil	SER/ARG-RELATED	NICLEAR MATRIX	PROTEIN	
		HMMER	1.8	HIMIMER	1.8	blastx.2			HMMER	1.8	HMMER	1.8	HMIMER	1.8	blastx.2				HMMER	1.8	blastx.14				blastx 2			
1		675		52		53			929		229		55		56				829						57	<u>`</u>		
		934216		921382		1155680			873441		862999		889416		1125258				948690						1224131	1014771		
		HCFCV92		HCFLIS4		HCFND04			HCFND04		HCHMV63		HCWDI 45		HCWEI19				HCWEI19						TICIMED 72	TCWND/		

2795	2759	2744	2741	2762	2744	2756	2913	2762	175	269	104	172	1/2	269	<u> </u>	236	2	3	246	(7		2124	325	
2613	2625	2616	2613	2631	2613	2673	2860	2631	134	912	202	77,	4 4	6	`	105	001	320	208		370	,00,	1936 2115	86	3
762	42%	34%	30%	28%	32%	32%	44%	31%	4.93	58%	33%		70.0	2005	2,40	306	3.00	44%	96'9		37%		%59 %09	40.7)
									PF00099	nir/T42650/T42650			PF00099	11 V D C 1 2 7 4 1 1	emolCAD013/4.1		PF00099	sp AAG02580 AAG0 2580	PF00099		sp 000549 000549		sp BAA91131 BAA9	1131	FF01/02
									PFAM: Zinc-binding	metallopiotease commin	,	human (fragment)	PFAM: Zinc-binding	metalloprotease domain	(AL133047) hypothetical	S	PFAM: Zinc-binding	TTYH1.	PFAM: Zinc-binding	metalloprotease domain	ORF2-LIKE PROTEIN	(FRAGMENT).	CDNA FLJ20378 FIS,	CLUINE NALAUSSU.	PFAM: Queuine tRNA- ribosyltransferase
									HMMER	1.8	olastx.2		HMMER	1.8	blastx.2		HMMER	blastx.2	HMMER	1.8	blastx.2		blastx.2		HMMER
									629		80		089				59		09	,			61		681
	<u>.</u>								200929		1125713		911314				691163		752975				1172240		954385
	, 						-		HCWKB72		HDDAF49		HDDAF49				HDPGQ74		RYSTIGUE	2000			HDPIX67		HDPIX67

86 313	99 146	98 958	496 534	13 873	137 166	122 355	227 268	49 75	426 391	441 112		144 185	320 364
35%	4.29	%\$6	13.41	%56	3.68	%6L	9.04	5.8	4.13	81%	100%	4.57	5.32
gi 2983726 gb AAC0 7288.1	PF00099	sp Q9Y6H3 Q9Y6H3	PF00099	gi 4867999 gb AAD3 1085.1 AF078164_1	PF00099	pir T50613 T50613	PF00099	PF00099	PF00099	вр[Q9UJH9]Q9UJH9		PF00099	PF00099
(AE000733) queuine tRNA-ribosyltransferase [Aquifex aeolicus]	PFAM: Zinc-binding metalloprotease domain	KU70-BINDING PROTEIN (FRAGMENT).	PFAM: Zinc-binding metalloprotease domain	(AF078164) Ku70- binding protein [Homo sapiens]	PFAM: Zinc-binding metalloprotease domain	hypothetical protein DKFZp547N213.1 - human (fragment)	PFAM: Zinc-binding metalloprotease domain	PFAM: Zinc-binding metalloprotease domain	PFAM: Zinc-binding metalloprotease domain	C380A1.2.1 (NOVEL	FROI EIN (ISOFORIM 1)).	PFAM: Zinc-binding metalloprotease domain	PFAM: Zinc-binding
blastx.14	HMMER 1.8	blastx.2	HMMER 1.8	blastx.14	HMMER 1.8	blastx.2	HMMER 1.8	HMMER 1.8	HMMER 1.8	blastx.2		HMMER 1.8	HMMER
•••	682	63	683		42		684	685	29			89	69
	915919	1136137	932212		508498		948687	851514	963673			915169	851009
	HDPXN01	HDQFT77	HDQFT77		HE2FR50		HE2SN25	HE8AE26	HEBGK01			HEFMB30	HEOPES8

			10	metallonrofease domain				
HETBR74	948667	70	HMMER	PFAM: Rhodanese-like	PF00581	32.2	321	461
			2.1.1	domain		/004	201	724
		<u></u>	blastx.2	ECIFICITY	sp 009112 DUS8_M	0%74	167	2 6
			_	PROTEIN	OUSE	54%	428	575
				PHOSPHATASE 8 (EC		25%	535	588
				3.1.3.48) (EU 1		7000	070	711
HFCAG94	1111177	71	blastx.2	PRO1722.	sp AAF69605 AAF69 605	62%	1008	850
11EC 4 C-04	735763	989	HMMER	PFAM: Zinc-binding	PF00099	3.92	100	129
ILCAU74		2	1.8	metalloprotease domain				
HFPHR82	957528	72	HMMER	PFAM: Actin	PF00022	91.7	1322	357
			2.1.1				, ,	200
			blastx.2	Uncharacterized	sp AAF67655 AAF67	100%	1523	6/7
				hypothalamus protein	955			
				HARP11.			1	1
HHFO084	857780	73	HMMER	PFAM: Zinc-binding	PF00099	4.21	141	101
-			1.8	metalloprotease domain		2007	000	36
HISAM68	1125189	74	blastx.2	CDNA FLJ20356 FIS,	sp BAA91112 BAA9 1112	%00I	667	C /
				CLOINE THE ISSEE:	0000000	3 48	178	198
HISAM68	868785	189	HMMER	PFAM: Zinc-binding	FF00099	2	3	
			1.0	metanoprotease comme	חסטטסםם	5 88	177	218
HLHDD45	942901	75	HMMER	PFAM: Zinc-binding	Fronoss	2	•	
			1.8	metalloprotease domain			000	100
HMMAR49	1087684	76	blastx.2	CDNA FLJ20378 FIS,	sp BAA91131 BAA9	%09	8/9	400
; 				CLONE KAIA0536.	1131	%0%	404	407
HMMAB49	462502	889	HIMMER	PFAM: Zinc-binding	PF00099	3.49	166	183
			1.8	metalloprotease domain				000
HMSG027	683031	11	blastx.2	Unnamed portein product.	sp BAB01630 BAB0 1630	%/5	295	369
					1030			

						%65	228	293
HMSG027	943946	689	HMMER 2.1.1	PFAM: Reprolysin (M12B) family zinc metalloprotease	PF01421	73.6	247	438
			blastx.2	(AF137335)	gb AAD25100.1	95%	232	462
				metalloprotease		% 86	18	245
				disintegrin cysteine-rich		35%	2	103
				protein, secreted form MDC-Ls [Homo sapiens]				
HNHAM52	457010	691	HMMER	PFAM: Zinc-binding	PF00099	3.5	72	68
			1.8	metalloprotease domain				
HNHEQ86	785580	79	HIMMER	PFAM: Zinc-binding	PF00099	3.9	7	48
			1.8	metalloprotease domain				
HNHHF46	859822	692	HIMMER	PFAM: Zinc-binding	PF00099	5.55	3	35
			1.8	metalloprotease domain				
HOECV83	653276	693	HIMMER	PFAM: Zinc-binding	PF00099	4.67	360	389
!			1.8	metalloprotease domain				
HORBO54	870674	82	HIMMER	PFAM: Zinc-binding	PF00099	5.64	277	300
			1.8	metalloprotease domain				
HOSFZ73	913876	694	HMMER	PFAM: Zinc-binding	PF00099	4.29	335	355
			1.8	metalloprotease domain				
HPIAU71	1123830	84	blastx.2	ethanolamine ammonia-	pir H65018 H65018	%86	400	89
				lyase (EC 4.3.1.7) heavy		%62	104	m
				chain - Escherichia coli		38%	278	516
				(strain K-12)				
HPIAU71	786811	695	HIMMER	PFAM: Zinc-binding	PF00099	3.49	265	291
			1.8	metalloprotease domain				
HRDBT72	1112136	85	blastx.2	PRO1722.	sp AAF69605 AAF69	73%	821	999
					905	15%	673	614
						27%	609	532

HRDBT72	507847	969	HMMER	PFAM: Zinc-binding metallonrotease domain	PF00099	7.31	295	324
HSDFT51	1124582	98	blastx.2	AMINOPEPTIDASE B	sp 009175 AMPB_R	33%	1291	872
				(EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) 1	AT			
HSDFT51	947918	269	HIMMER	PFAM: Zinc-binding	PF00099	6.14	328	363
			1.8	metalloprotease domain				
			blastx.14	aminopeptidase-B [Rattus	gil1754515 dbj BAA1	31%	94	306
	7			norvegicus]	3413.1	36%	289	420
HSDJM56	948669	87	HMMER	PFAM: Zinc-binding	PF00099	6.46	114	149
			1.8	metalloprotease domain				
			blastx.2	formate C-	pir S01788 S01788	%66	811	395
	,			acetyltransferase (EC		%66	395	m
				2.3.1.54) 1 - Escherichia				
				coli				
HSICX21	531267	88	HMMER	PFAM: Zinc-binding	PF00099	3.8	307	336
			1.8	metalloprotease domain				
HSIDS82	531248	68	HMMER	PFAM: Zinc-binding	PF00099	5.91	706	238
			1.8	metalloprotease domain				
HSNAH21	571314	8	HIMMER	PFAM: Zinc-binding	PF00099	7.14	91	135
			1.8	metalloprotease domain				
HSODC08	966264	91	HMMER	PFAM: Zinc-binding	PF00099	14.78	551	510
			1.8	metalloprotease domain				
	<u> </u>		blastx.2	BM-014.	sp AAF64270 AAF64 270	94%	779	222
HSPAB58	736098	92	HMMER	PFAM: Zinc-binding	PF00099	4.6	39	98
			1.8	metalloprotease domain			i d	
HSOCM85	963554	93	HIMMER	PFAM: Zinc-binding	PF00099	5.37	187	731
,	_		1.8	metalloprotease domain				18
HTOTA82	844319	94	HMMER	PFAM: Zinc-binding	PF00099	4.25	20	82
111 000 000	2					•		

	661	2155			1525	3	747	367		367	-		998	971	539	708	618	985	532	803	2130	753	614	999	2176	711	2177
	23	2			1731	00,	198	200	•	200			1246	1150	703	791	791	1113	840	994	2216	995	682	703	2241	191	2215
	378.5	51%			52%		4.43	79.5		%96			48%	63%	54%	78%	20%	55%	38%	48%	62%	37%	%09	34%	63%	57%	84%
	PF01433	sp Q9UKY2 Q9UKY	2		sp BAA91131 BAA9	1131	PF00099	PF01433		sp Q9UKY2 Q9UKY	2		sp O60448 O60448														
metalloprotease domain	PFAM: Peptidase family M1	POCYTE-DERIVED		AMINOPEPTIDASE.	CDNA FLI20378 FIS,	CLUNE KALAU350.	PFAM: Zinc-binding metalloprofesse domain	PFAM: Pentidase family		TE-DERIVED		AMINOPEPTIDASE.	NEURONAL THREAD	PROTEIN AD7C-NTP.													
1.8	HMMER 2.1.1	blastx.2			blastx.2		HIMMER 1.8	HAMMER	2.1.1	blastx.2			blastx.2														
	95				96		869	0.7	<u> </u>				86	· ·													
	931155				1145916		662347	047015	74(717				1156447))													
	HUUDH57				HWACV74		HWACV74	TYNY A EXIZO	II WAL W39				HWRRR65	20017771111													

PFAM: Zinc-binding PF00099 4.15 1129 118 1							32%	972	962
Table Tabl							470%	1129	1061
1,47723 699 HMMER PFAM: Zinc-binding PF00099 717% 6140 2 717% 2140 2 747723 699 HMMER PFAM: Matrixin PF00013 4.15 185 1.8			-				46%	2183	2100
747723 699							40%	909	532
747723 699 HMMER PFAM: Zinc-binding PF00099 4.15 185							37%	625	521
747723 699 HMMER PFAM: Zinc-binding PF00099 4.15 185 5 969190 99 HMMER PFAM: Matrixin PF00413 45.6 17 6 2.1.1 HAMER PFAM: Matrixin PF00413 45.6 17 920850 100 HMMER PFAM: Matrixin PF0 21.1 920850 100 HMMER PFAM: 35-cyclic PF00233 195.7 187 101 HMMER PFAM: 35-cyclic-AMP pir/A47286/A47286 90% 1 101 HMMER PFAM: 35-cyclic-AMP pir/A47286/A47286 90% 1 101 HMMER PFAM: Aconitase (EC 3.14-1-1 human 45.9 15 102 103 HMMER PFAM: Aconitase family PF00330 72.2 228 101 HMMER PFAM: Aconitase family PF00330 72.2 228 101 HMMER PFAM: Aconitase family PF00330 15 101 HMMER PFAM: Aconitase							71%	2140	2099
1.0 HMMER PFAM: Matrixin PF00413 45.6 17	65	747723	669	HMMER	PFAM: Zinc-binding	PF00099	4.15	185	205
Diastr.2 HATCHING ENZYME SplP91953 HE_HEM 51% 2		969190	66	HMMER	PFAM: Matrixin	PF00413	45.6	17	109
PRECURSOR (EC PU				blastx.2	HATCHING ENZYME	sp P91953 HE HEM	51%	2	304
920850 100 HMMER PFAM: 3'S'-cyclic PF00233 195.7 187 2.1.1 nucleotide phosphodiesterase 90% 1 blastx.2 3',5'-cyclic-AMP pir[A47286]A47286 90% 1 phosphodiesterase (EC 3.1.4) - human 3.1.4) - human 72.2 228 786337 101 HMMER PFAM: Aconitase family PF00330 72.2 228 2.1.1 (aconitate hydratase) sp[Q99798]ACON_H 61% 15 HYDRATASE, UMAN UMAN 15 HYDRO-LYASE) (ACONITASE) HYDRO-LYASE) (ACONITASE) (ACONITASE) (ACONITASE) (ACONITASE) (ACONITASE) (ACONITASE)					PRECURSOR (EC	PU			
920850 100 HMMER PFAM: 3'S'-cyclic PF00233 195.7 187 2.1.1 phosphodiesterase Blastx.2 3',S'-cyclic-AMP pir[A47286]A47286 90% 1 phosphodiesterase (EC 3.1.4) - human (fragment) PF00330 72.2 228 786337 101 HMMER PFAM: Aconitase family PF00330 72.2 228 2.1.1 (aconitate bydratase) sp Q99798 ACON_H 61% 15 MITOCHONDRIAL PRECURSOR (EC 42.1.3) (CITRATE HYDRO-LYASE) HYDRO-LYASE) HYDRO-LYASE) (ACONITASE) HYDRO-LYASE) 6ACONITASE) 91% 69					3.4.24.12) (HE) (HEZ) 1				
2.1.1 nucleotide phosphodiesterase blastx.2 3,5'-cyclic-AMP phosphodiesterase (EC 3.1.4) - human (fragment) 786337 101 HMMER PFAM: Aconitase family PF00330 2.1.1 (aconitate hydratase) blastx.2 ACONITATE PRECURSOR (EC 4.2.1.3) (CITRATE HYDRO-LYASE) HYDRO-LYASE) (ACONITASE) (ACONITASE) 102 blastx.2 aconitate hydratase (EC pirlG64875 G64875 91% 69		920850	100	HMMER	PFAM: 3'5'-cyclic	PF00233	195.7	187	789
phosphodiesterase pir A47286 A47286 90% 1 phosphodiesterase (EC 3.14) - human (fragment) PF00330 72.2 228 2.1.1				2.1.1	nucleotide				
blastx.2 3',5'-cyclic-AMP pir A47286 A47286 90% 1 phosphodiesterase (EC 3.1.4) - human (fragment) (fra			-		phosphodiesterase				
Phosphodiesterase (EC 3.1.4) - human (fragment) 786337 101 HMMER PFAM: Aconitase family PF00330 72.2 228 2.1.1 (aconitate hydratase) sp Q99798 ACON_H 61% 15 HYDRATASE, UMAN				blastx.2	3',5'-cyclic-AMP	pir[A47286]A47286	%06	1	804
3.1.4) - human					phosphodiesterase (EC				
786337 HMMER PFAM: Aconitase family PF00330 72.2 228 2.1.1 (aconitate hydratase) sp Q99798 ACON_H 61% 15 HYDRATASE, UMAN 15 MITOCHONDRIAL PRECURSOR (EC 4.2.1.3) (CITRATE HYDRO-LYASE) HYDRO-LYASE) (ACONITASE). (ACONITASE). 1217181 102 blastx.2 aconitate hydratase (EC pir G64875 G64875 91% 69					3.1.4) - human				
786337 101 HMMER PFAM: Aconitase family PF00330 72.2 228 2.1.1 (aconitate hydratase) sp Q99798 ACON_H 61% 15 HYDRATASE, UMAN 15 MITOCHONDRIAL PRECURSOR (EC 4.2.1.3) (CITRATE HYDRO-LYASE) HYDRO-LYASE) (ACONITASE). 1217181 102 blastx.2 aconitate hydratase (EC pir G64875 G64875 91% 69					(fragment)				
2.1.1 (aconitate hydratase) splQ99798 ACON_H 61% 15 blastx.2 ACONITATE splQ99798 ACON_H 61% 15 HYDRATASE, UMAN MITOCHONDRIAL PRECURSOR (EC 4.2.1.3) (CITRATE HYDRO-LYASE) HYDRO-LYASE) (ACONITASE). (ACONITASE). 217181 102 blastx.2 aconitate hydratase (EC pir G64875 G64875 91% 69	360	786337	101	HMMER	PFAM: Aconitase family	PF00330	72.2	228	353
blastx.2				2.1.1	(aconitate hydratase)				
HYDRATASE, UMAN HYDRATASE, UMAN				blastx.2	ACONITATE	sp Q99798 ACON_H	%19	15	353
MITOCHONDRIAL PRECURSOR (EC 4.2.1.3) (CITRATE HYDRO-LYASE) (ACONTTASE) (ACONTTASE) aconitate hydratase (EC pir G64875 G64875 91% 69	-				HYDRATASE,	UMAN			
PRECURSOR (EC					MITOCHONDRIAL				
4.2.1.3) (CITRATE					PRECURSOR (EC				
HYDRO-LYASE)					4.2.1.3) (CITRATE		_		
(ACONITASE). (ACONITASE).	-				HYDRO-LYASE)				
1217181 102 blastx.2 aconitate hydratase (EC pir/G64875/G64875 91% 69					(ACONITASE).				
	32	1217181	102	blastx.2	aconitate hydratase (EC	pir G64875 G64875	91%	69	887

				4.2.1.3) - Escherichia coli				
HDPDE32	973342	700	HIMMER	PFAM: Aconitase family (aconitate hydratase)	PF00330	260.7	219	569
HBDAC79	1199232	103	blastx.2	A B	sp Q9UKU7 Q9UKU	%98 %46	196	528 203
				PRECURSOR (CDNA		45%	452	583
				FLJ20352 FIS, CLONE				
				HEP14524).		0.00	3	5
HBDAC79	935414	701	HMMER	PFAM: Acyl-CoA	PF00441	102.6	46	342
			1.1.4	(AT 021058) fed E0	oil2911026lemblCAA	62%	94	255
			DIASUA.14	(ALOZ1909) James [Mycobacterium	5/2719.1	51%	250	384
				theresis		64%	348	422
				faround		35%	9	89
HEMDX48	1163778	104	blastx.2	ACYL-COA	sp P50544 ACDV_M	48%	175	1917
				DEHYDROGENASE,	OUSE			
				VERY-LONG-CHAIN				-
		_		SPECIFIC, 1				,
HEMDX48	521844	702	HMMER	PFAM: Acyl-CoA	PF00441	115.91	4	321
			1.8	dehydrogenases				,
HHASB48	721150	105	HIMMER	PFAM: Acyl-CoA	PF00441	101.3	319	645
			2.1.1	dehydrogenase				
			blastx.2	ACYL-COA	sp[P50544 ACDV_M	54%	175	648
				DEHYDROGENASE,	HSOO H			
				VEKI-LONG-Cham				
	110170	106	1-10-04r 2	OFFULLIC, I	nir[D83326[D83326	62%	359	979
HLWCA!/	1104/07	700	Oldata.2	dehydrogenase PA2550				
				[imported] - Pseudomonas				
				aeruginosa (strain PAO1)				

HLWCA17	957664	703	HMMER	PFAM: Acyl-CoA	PF00441	52.61	521	892
			1.8	dehydrogenases				
			blastx.14	(AL096811) putative acyl-	gi 5441764 emb CAB	23%	521	904
				CoA dehydrogenase	46788.1	28%	286	519
				[Streptomyces coelicolor				
		1		A5(2)]	000100000000000000000000000000000000000	7007		000
HNTTD09	1104487	107	blastx.2	K09H11.1 PROTEIN.	065100 065100 ds	32%	1/9	832 152
HNTTD09	676665	704	HMMER	PFAM: Acyl-CoA	PF00441	49.76	09	425
			1.8	dehydrogenases		,		
HSKDT07	927823	108	HMMER	PFAM: Acyl-CoA	PF00441	122.42	13	369
			1.8	dehydrogenases	,			
			blastx.2	ACYL-COA	spiP50544 ACDV_M	38%	7	906
	_			DEHYDROGENASE,	OUSE			-
				VERY-LONG-CHAIN	•			
	-			SPECIFIC, 1				
HSRDB26	1102231	109	blastx.2	acyl CoA dehydrogenase	pir I41124 I41124	%66	305	658
				homolog - Escherichia		72%	27	305
				coli		81%	2	34
HSRDB26	525475	705	HIMMER	PFAM: Acyl-CoA	PF00441	115.7	21	290
			2.1.1	dehydrogenase				
HAPBS07	967325	110	HIMMER	PFAM: Alcohol/other	PF00106	50.05	19	267
			1.8	dehydrogenases, short				
				chain type				
			blastx.2	RETINOL	sp Q9Y2P9 Q9Y2P9	75%	317	682
				DEHYDROGENASE		%69	61	306
				HOMOLOG.		62%	280	708
						34%	561	683
HAUAI17	921674	111	HMMER	PFAM: short chain	PF00106	198.7	172	289
			7.1.1	uciliyai ogonaso				

			blastx.2	RETINAL SHORT-	sp Q9UKU3 Q9UKU	81%	145	687
				CHAIN	3	100%	289	857
			•	DEHYDROGENASE/RE		_		
				DUCTASE RETSDR3.				
HBCBT19	959953	112	HIMMER	PFAM: short chain	PF00106	30.7	202	417
			2.1.1	dehydrogenase				
			blastx.2	hypothetical protein	pir/T04022/T04022	40%	214	552
				F17A8.100 - Arabidopsis		41%	38	196
در				thaliana		52%	591	653
HBCPT10	957631	113	HMMER	PFAM: Alcohol/other	PF00106	78.87	338	673
			1.8	dehydrogenases, short			-	
				chain type				
			blastx.2	CDNA FLJ11008 FIS,	sp BAA91953 BAA9	%16	263	029
				CLONE PLACE1003100,	1953	%08	671	838
				MODERATELY		•	•	
				SIMILAR 1				
HBGDA14	866258	114	HMMER	PFAM: Alcohol/other	PF00106	127.15	33	299
			1.8	dehydrogenases, short				
-				chain type				
			blastx.2	2,3-dihydro-2,3-	pir A91904 DEECDB	%26	m	482
				dihydroxybenzoate			-	
				dehydrogenase (EC				
				1.3.1.28) - Escherichia				
				coli		id.		
HCHNJ32	934848	115	HMMER	PFAM: short chain	PF00106	213.6	54	587
			2.1.1	dehydrogenase				
			blastx.2	CARBONYL	SHU90HYY9 Q9UHYY	%56	33	764
				REDUCTASE.	9			
HCHON59	931082	116	HMMER	PFAM: SCP-2 sterol	PF02036	96.3	1006	1335
			2.1.1	transier family				

			blastx.2	CG5590 PROTEIN.	sp Q9VB10 Q9VB10	47%	538	1344
HCUGN19	716989	117	HMMER	PFAM: Alcohol/other	PF00106	8.05	86	151
			1.8	dehydrogenases, short chain type				
HCUGR38	706471	118	HMMER	PFAM: Alcohol/other	PF00106	73.02	102	284
	,		1.8	dehydrogenases, short chain type				
		•	blastx.2	Putative oxidoreductase.	sp CAB94622 CAB9 4622	55% 30%	105	296
HDPND85	852628	119	HMMER	PFAM: Alcohol/other	PF00106	191.2	113	709
	-		1.8	dehydrogenases, short chain type				
			blastx.2	CG9360 PROTEIN.	sp Q9VYU9 Q9VYU	42%	113	841
HDPRN38	883658	120	HMMER	PFAM: Alcohol/other	PF00106	175.59	123	089
			1.8	dehydrogenases, short chain type				
			blastx.2	Peroxisomal trans 2-enoyl	sp AAF69798 AAF69	81%	111	824
				CoA reductase (EC 1.3.1.8).	798	84%	61	138
HE8AM92	952610	121	HMMER	PFAM: Alcohol/other	PF00106	86.8	202	330
			1.8	dehydrogenases, short				
				chain type				
			blastx.2	DTDP-4-KETO-6-	sp Q9UJ54 Q9UJ54	%06	208	654
				DEOXY-D-GLUCOSE 4-				
				REDUCTASE.				
HE9RE21	888243	122	HMMER	PFAM: short chain	PF00106	81.3	96	386
			2.1.1	dehydrogenase	٠			
			blastx.2	ESTRADIOL 17 BETA-	sp P56937 DHB7_H	100%	96	419

522	881		998		260		260	426	322	67	285			441	551	361		5	283		000	282	•	,	648
421	300		294		09		48	322	257	2	109			139	456	23			707	_		19			367
%88	137.09		54%		55.01		83%	100%	%56	81%	11.34			%66	75%	100.69			%86			25.77			53%
UMAN	PF00106		sp O57314DHBX_A	יי ועזען	PF00106		YHU9019YHU901as	6			PF00106			sp AAG09721 AAG0	9721	PF00106			sp Q9Y6G8 Q9Y6G8			PF00106			pir/T04022/T04022
DEHYDROGENASE 7	PFAM: Alcohol/other	dehydrogenases, short chain type	PUTATIVE STEROID	SPM2 (EC 1.1.1).	PFAM: Alcohol/other	dehydrogenases, short	VI.	, m			PFAM: Alcohol/other	dehydrogenases, short	chain type	HSCARG.		PFAM: Alcohol/other	dehydrogenases, short	chain type	STEROID	DEHYDROGENASE	HOMOLOG.	PFAM: Alcohol/other	dehydrogenases, short	chain type	hypothetical protein
	HMMER	1.8	blastx.2		HMMER	1.8	hlactx 7	7.112			HMMER	1.8		blastx.2		HMMER	1.8		blastx.2			HIMMER	1.8		blastx.2
	123				124						125					126						127			
	884009				840939						856590					914083						959954			
	HETKH30				HHAME78						HKABI68					HKMLN95						HMCFA91			

				F17A8.100 - Arabidopsis		41%	_	7.87
				thaliana				
HNTBF75	836701	128	HMMER	PFAM: short chain	PF00106	35.2	202	321
			2.1.1	dehydrogenase				
			blastx.2	STEROID	8D9Y6G8 Q9Y6G8	78%	52	414
				DEHYDROGENASE				
				HOMOLOG.				
HPTGB43	726460	129	HMMER	PFAM: short chain	PF00106	45.1	84	191
			2.1.1	dehydrogenase				
			blastx.2	CARBONYL	YHU90 9YHU90 qs	73%	87	374
				REDUCTASE.	6			
HPTVL90	509487	130	HMMER	PFAM: short chain	PF00106	46.3	11	115
			2.1.1	dehydrogenase				
			blastx.2	RETINAL SHORT-	sp Q9UKU3 Q9UKU	1,%92	∞	319
					3	-		_
				DEHYDROGENASE/RE				
				DUCTASE RETSDR3.				
HSKIA89	837986	131	HMMER	PFAM: Alcohol/other	PF00106	17.7	359	478
			1.8	dehydrogenases, short				
				chain type				
			blastx.2	hypothetical protein	pir/T24832/T24832	45%	329	619
				TiiF9.11 -		23%	123	320
				Caenorhabditis elegans		35%	737	820
HTXGF27	992269	132	HMMER	PFAM: short chain	PF00106	208.7	193	765
			2.1.1	dehydrogenase				
			blastx.2	hypothetical protein	pir/T17307/T17307	93%	70	1011
				DKFZp5660084.1 -		100%	38	73
٠			•	human				
HWHHW54	684125	133	HMMER	PFAM: short chain	PF00106	59.1	871	1002
	· 		2.1.1	dehydrogenase				

1059	664	664	260	417		450	134	588		735		306		333	359			564	655		323
871	257	257	186	193		184	36	163		16		133		58	309			64	554		3
77%	101.3	74%	64%	44.2		%56	84%	113.24		82%		46.57		83%	94%			91%	19%	-	141.1
sp AAF80754 AAF80 754	PF00106	sp Q9Y391 Q9Y391		PF00106		sp Q9Y2P9 Q9Y2P9		PF00106		sp CAB92744 CAB9	t+/7	PF00106		sp BAA91953 BAA9	1953			pir A33276 DEECTH			PF00107
Oxidoreductase UCPA.	PFAM: short chain dehydrogenase	CGI-82 PROTEIN.		PFAM: Alcohol/other	denydrogenases, snort chain type	RETINOL	DEHYDROGENASE HOMOLOG.	PFAM: Alcohol/other	dehydrogenases, short chain type	C359F1.1 (novel protein	(ortholog of mouse and far	PFAM: Alcohol/other	dehydrogenases, short chain type	CDNA FLJ11008 FIS,	CLONE PLACE1003100,	MODERATELY	SIMILAR 1	L-threonine 3-	dehydrogenase (EC	1.1.1.103) - Escherichia coli	PFAM: Zinc-binding
blastx.2	HMMER 2.1.1	blastx.2		HMMER	1.0	blastx.2		HMMER	1.8	blastx.2		HMMER	1.8	blastx.2				blastx.2			HMMER
	134			135				136				137						138			902
	857383			967326				925331				957630						1103922			786307
	HWHPO29			HWLPR94				HWLUL28				HWLXT48						HBGMD15			HBGMD15

	231	318			595		388		994		655		510				283		836	190	471		480	738	798
	76	9/			74		5		2		344		88				152		309	14	265		193	535	733
	28.74	95%			87%		236		%56		76.21		%16				30.97		%86	72%	53.56		15%	75%	63%
	PF00107	pir F64794 F64794			pir D64763 D64763		PF00107		pir D64880 D64880		PF00107		pir F64794 F64794				PF00107		sp Q9Y373 Q9Y373		PF00107		sp 009125 009125		,
dehydrogenases	PFAM: Zinc-binding dehydrogenases	probable alcohol	dehydrogenase (EC 1.1.1.1) ybdR -	Escherichia coli	alcohol dehydrogenase	(EC 1.1.1.1) C - Escherichia coli	PFAM: Zinc-binding	dehydrogenases	probable oxidoreductase	(EC 1.1.1) yejQ -	PFAM: Zinc-hinding	dehydrogenases	probable alcohol	dehydrogenase (EC	1.1.1.1) ybdR-	Escherichia coli	PFAM: Zinc-binding	dehydrogenases	CGI-63 PROTEIN.		PFAM: Zinc-binding	dehydrogenases	ALDO-KETO	REDUCTASE.	
2.1.1	HMMER 1.8	blastx.2			blastx.2		HMMER	2.1.1	blastx.2		HWMFR	1.8	blastx.2				HMMER	1.8	blastx.2		HMMER	1.8	blastx.2		
	139				140		707		141		708	2	142				709		143		710		144		
	789744				1103672		730927		1103524		873083	20020	1105422				866274		1152110		633682		1105538		
	HNGMA91				HSLEI57		HSI.EI57		HSLFE21		LIGI FEO 1	ו אינו זינונון	HSLE 40				HSLE40		HTXHA35		HTXHA35		HAICS07		

gi[1698718 gb AAB3 76% 7274.1 91% 91% 85% 85% 85%	reductase family	2.1.1 blastx.14
75064 AAF75	3 6	aldo-ket
75064 AAF75	reductase [Mus	misciplis
AF75064 AAF75		
	Acetyl-CoA synthetase.	Acetyl-(
PF00501 249.5	PFAM: AMP-binding	PFAM:
		enzyme
gi 608694 emb CAA8 65% 6738.11	acetyl-CoA synthetase Drosonhila melanogaster	acetyl-Co
splCAB75500 CAB7 98%	\vdash	DJ568C1
\$500 100%		binding er
PF00501 43.02	PFAM: AMP-binding	PFAM: A
		enzymes
sp CAC07591 CAC0 99% 7591	from Patent	Sequence 17 WO9951740
PF00501 19.17	PFAM: AMP-binding enzymes	PFAM: A enzymes
gi 2612939 gb AAC6 90%	(AF023258) fatty acid	(AF02325
9640.1	orotein [Mus	transport produced in the prod
pirF83345F83345 75%	probable non-ribosomal	probable 1
74%		peptide synthetase
37%	PA2402 [imported] -	PA2402 [
31%	Pseudomonas aeruginosa	Pseudomo
57%	(01)	(strain PAO1
53%		,
PF00501 69.62	PFAM: AMP-binding	PFAM: 4

	069	778	785	555		069	778	785	1182	200	1208	407		516		654	1111	579	846	1096	556	901	9	949	781	484	1099	568
	85	999	705	316		85	995	705	502	Э	1146	39		334		124	31	295	748	959	65	98		764	647	365	896	491
	84%	81%	25%	82.8		84%	81%	55%	93%	97%	57%	35.92		18.6		%19	85%	34%	54%	48%	41%	91.1		51%	48%	25%	36%	%05
	sp Q9UJ15 Q9UJ15			PF00501		emb CAB61786.1			sp BAA91273 BAA9	1273		PF00501		PF00501		sp AAF64300 AAF64	300			sp BAB02683 BAB0	2683	PF00501		gi 699196 gb AAA62	961.1		-	
enzymes	DJ18C9.1 (SIMILAR TO	ACETYL-COENZYME	A SYNTHETASE) 1	PFAM: AMP-binding	enzymes	(AL049709) dJ18C9.1	(similar to acetyl-	coenzyme A synthetase) [Homo sapiens]	CDNA FLJ20581 FIS,	CLONE REC00491.		PFAM: AMP-binding	enzymes	PFAM: AMP-binding	enzymes	Hypothetical 179.7 kDa	protein.			Long-chain-fatty-acid-	CoA ligase-like protein.	PFAM: AMP-binding	enzymes	4-coumarate-coA ligase	[Mycobacterium leprae]			
1.8	blastx.2			HMMER	1.8	blastx.2			blastx.2			HMMER	1.8	HMMER	1.8	blastx.2				blastx.2		HMMER	1.8	blastx.14				
	149			716					150			717		151						152		718						
	1182322			852622					1203140			887490		839719						1104119		923824						
	HDQDY52	,		HDQDY52					HEEAA32			HEEAA32		HEGAN70						HFKMF42		HFKMF42						

103	623	291	449	232		220	1961		453		481		571	681	1011	694		931			536			324	324
65	570	55	384	53		7	561				17		17	586	16	68		2	-		6	-		101	19
53%	44%	%86	31%	99		%06	%66		115.4		103.84		%68	57%	74%	104.64		78%			%96	_		2000	20.33
		pir H64791 YGECEF		PF00501		gi 145843 gb AAA92 015.1	sp CAB75500 CAB7	5500	PF00501		PF00501		spBAA91273BAA9	1273	sp[O70490]O70490	PF00501		gj3127193 gb AAD0	5209.1		sp Q9Y2P5 Q9Y2P5			10000000	PF00501
		enterobactin synthetase	component F - Fscherichia coli	PFAM: AMP-binding	enzyme	enterobactin [Escherichia coli]	DI568C11.3 (novel AMP-	binding enzyme similar to	PFAM: AMP-binding	enzyme	PFAM: AMP-binding	enzymes	CDNA FLJ20581 FIS,	CLONE REC00491.	KIDNEY-SPECIFIC PROTEIN.	PFAM: AMP-binding	enzymes	(AF062389) kidney-	specific protein [Rattus	norvegicus]	VERY LONG-CHAIN	ACYL-COA	SYNTHETASE	HOMOLOG 2.	PFAM: AMP-binding
		blastx.2		HMMER	2.1.1	blastx.14	blastx.2		HMMER	2.1.1	HIMMER	1.8	blastx.2		blastx.2	HMMER	1.8	blastx.14			blastx.2				HMMER
		153		719			154		720		155				156	721					157				722
		1104964		933802			1227613		574897		466567				1106225	969544	_				1107517				837030
_		нгрн С06		HFPHG06			HHEMB89		HHEMB89		HLDPC46				HLDRG44	HLDRG44					HLICR73				HLICR73

			1.8	enzymes				
			blastx.2	(AF064255) very long- chain acyl-CoA synthetase	gb AAD29444.1 AF0 64255 1	99%	1 450	441
				homolog 2; VLCS-H2 [Homo sapiens]	l			
HNHOP64	1103943	158	blastx.2	FATTY ACID TRANSPORT PROTEIN	sp O95186 O95186	%06	515	57
HNHOP64	966754	723	HMMER	PFAM: AMP-binding	PF00501	23.65	539	757
			1.8	enzymes				
			blastx.14	(AF055899) fatty acid	gi 4206376 gb AAD1	%88	374	835
				transport protein [Homo	1623.1	52%	835	891
HSDEF56	1128288	159	blastx.2	acetateCoA ligase (EC	pir D65215 D65215	%16	106	729
				6.2.1.1) - Escherichia coli	-	95%	707	892
				`		100%	268	986
HSDEF56	496551	724	HMMER	PFAM: AMP-binding	PF00501	175.3	2	436
			2.1.1	enzyme				
HTENI29	1105518	160	blastx.2	LONG-CHAIN ACYL- COA SYNTHETASE 5.	sp Q9UKU0 Q9UKU 0	%16	24	1172
HTENIZ9	954519	725	HMMER	PFAM: AMP-binding	PF00501	99	396	845
			1.8	enzymes				
			blastx.14	(AF129166) long-chain	gi 5702202 gb AAD4	%86	51	1172
				acyl-CoA synthetase 5 [Homo sapiens]	7199.1 AF129166_1			
HWMKD72	1106729	161	blastx.2	agmatinase PA1421	pir H83468 H83468	64%	2	643
				[imported] - Pseudomonas		•		-
				aeruginosa (strain PAO1)				
HWMKD72	970613	726	HMMER	PFAM: Arginase family	PF00491	179.6	11	565
			2.1.1					
			blastx.14	agmatine ureohydrolase	gi 882466 gb AAA69	48%	302	625

				[Escherichia coli]	104.1	20%	14	166
						44%	164	271
HAPSQ21	972037	162	HMMER	PFAM: Eukaryotic	PF00026	274.4	211	735
			2.1.1	aspartyl protease				
			blastx.2	NAPSIN 1 PRECURSOR	sp 096009 NAP1 H	100%	58	762
				(EC 3.4.23) (NAPSIN	UMAN	%06	797	865
				A) (NAPA) 1				
HLJDW02	1192885	163	blastx.2	NAPSIN 1 PRECURSOR	sp 096009 NAP1_H	92%	3	569
				(EC 3.4.23) (NAPSIN	UMAN			
				A) (NAPA) 1				
HLJDW02	837592	727	HMMER	PFAM: Eukaryotic	PF00026	134.5	65	412
			2.1.1	aspartyl protease	:			-
			blastx.2	(AF090386) napsin A	gb[AAD04917.1]	100%	47	433
				[Homo sapiens]		65%	433	534
HIMGBT01	1205666	164	blastx.2	aspartic proteinase (EC	pir A59090 A59090	100%	3	1073
			,	3.4.23) BACE precursor		%58	1705	1992
				- human				-
HMGBT01	879904	728	HMMER	PFAM: Eukaryotic	PF00026	31.46	3	362
			1.8	aspartyl proteases				
HSSJJ24	1178041	165	blastx.2	aspartic proteinase (EC	pir A59090 A59090	100%	∞	1081
				3.4.23) BACE precursor		%58	1714	2001
				- human				
HSSJJ24	905092	729	HMMER	PFAM: Eukaryotic	PF00026	26.48	33	113
			1.8	aspartyl proteases	:			
HFTCG46	669383	166	HMMER	PFAM: Eukaryotic-type	PF00194	101.7	78	266
			2.1.1	carbonic anhydrase				-
			blastx.2	CARBONIC	sp Q9Y2D0 CA5B_H	%86	78	257
				ANHYDRASE VB,	UMAN			
	-			MITOCHONDRIAL				
				PRECURSOR (EC 1				-

16 249		19 369		434 499	_		88 3331	2 265		1 315	1 345	168 260	73 195				64 195			270 332				2 301	
							% 2888	192		96	%						_				•			15	
84.3		%69	%69	%06		%66	%26	19		69.36	64%	%96	100%				79.8	: -	%59	%56				55.15	
PF00194		sp Q9ULX7 CAHE	HUMAN			sp Q9R7S7 Q9R7S7		PF00285		PF00285	pir G64807 YKEC		pir/JE0193/JE0193				PF00346		pir F83342 F83342					PF00122	
PFAM: Eukaryotic-type	carbonic anhydrase	CARBONIC	ANHYDRASE XIV	PRECURSOR (EC	4.2.1.1) (CARBONATE 1	OUTER MEMBRANE	USHER PROTEIN PMFC PRECURSOR.	PFAM: Citrate synthase		PFAM: Citrate synthase	citrate (si)-synthase (EC	4.1.3.7) - Escherichia coli	NADH dehydrogenase	(ubiquinone) (EC 1.6.5.3)	chain NDUFS2 precursor	- human	PFAM: Respiratory-chain	Kd subunit	probable cation-	transporting P-type	ATPase PA2435	[imported] - Pseudomonas	aeruginosa (strain PAO1)	PFAM: E1-E2 ATPases	
HIMMER	2.1.1	blastx.2				blastx.2		HMMER	2.1.1	HMMER 1.8	blastx.2		blastx.2				HMMER	7.1.1	blastx.2				-	HIMMER	1.8
167						168		730		169			170				731		171					732	
929511						1174334		573965		506599			1128095				764970		1172460					853009	
HNTMD81						HBSAJ60		HBSAJ60		HSKCI43			HSDKE47	-			HSDKE47		HCWTB56					HCWTB56	

				protein [Lactococcus				
HFPBS73	1144027	172	blastx.2	F-exchanging se (EC 3.6.1.36)	pir H64804 PWECB K	81%	373	1122
				chain B [validated] - Escherichia coli				
HFPBS73	954892	733	HMMER 2.1.1	PFAM: E1-E2 ATPase	PF00122	196.5	3	572
			blastx.2	kdpB [Escherichia coli]	gb AAB96336.1	100%	580	563
HOEDD44	954893	173	HMMER 2.1.1	PFAM: E1-E2 ATPase	PF00122	173.2	53	574
			blastx.2		pir H64804 PWECB	95%	53	574
				ATPase (EC 3.6.1.36)	∀	39%	513	635
				Escherichia coli				
HSUAN33	956315	174	HMMER 1.8	PFAM: E1-E2 ATPases	PF00122	46.29	1317	907
			blastx.2	Hypothetical 128.8 kDa protein.	sp CAB89728 CAB8 9728	48% 35%	1596 693	766 256
HBCMD49	1206021	175	blastx.2	hypothetical protein F38H4.8 - Caenorhabditis	pir T21981 T21981	44%	46	357
				elegans		1	000	650
HBCMD49	865314	734	HMMER	PFAM: Enoyl-CoA	PF00378	74.0	507	000
	-		2.1.1	hydratase/isomerase family				
			blastx.2	(AE000989) enoyl-CoA	gb AAB89601.1	39%	197	619
				hydratase (fad-4) Archaeoglobus fulgidus				
HKABN12	956826	176	HMMER	PFAM: Enoyl-CoA	PF00378	31.8	900	820

	593 739	2586	268	355 495	2090	274	2074	1757	498
	745	1297	5	334	1701	167	1685	1635	97
	37%	93%	159.1	%06 %88	%66	32.87	%86	39.5	%68
,	sp Q9V7Y3 Q9V7Y3	pir F64890 F64890	PF00378	gi 2764828 emb CAA 66095.1	sp BAA91922 BAA9 1922	PF00378	sp BAA91922 BAA9 1922	PF00378	spBAA91922 BAA9 1922
hydratase/isomerase family	CG6984 PROTEIN.	probable 3- hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) ydbU - Escherichia coli (strain K-	PFAM: Enoyl-CoA hydratase/isomerase	enoyl-CoA hydratase	CDNA FLJ10948 FIS, CLONE PLACE1000142, WEAKLY SIMILAR TO	PFAM: Enoyl-CoA hvdratase/isomerase	CDNA FLJ10948 FIS, CLONE PLACE1000142, WEAKLY SIMILAR TO	PFAM: Enoyl-CoA hydratase/isomerase	CDNA FLJ10948 FIS, CLONE PLACE1000142,
2.1.1	blastx.2	blastx.2	HMMER 2.1.1	blastx.14	blastx.2	HMMER	blastx.2	HMMER 2.1.1	blastx.2
	_1	177	735		178	736	179	737	180
		1228291	920386		1204710	791284	1228151	863712	1228152
		HMOAC31	HMOAC31		НМУВ 092	HMVBQ92	HOELA62	HOELA62	HSSGE35

	N	WEAKLY SIMILAR TO				
HMMER PFA	17 P	PFAM: Enoyl-CoA hvdratase/isomerase	PF00378	39.59	70	210
blastx.14 AU	10	AU-binding	gil780241 emb CAA5	57%	88	357
pro	0	protein/Enoyl-CoA	6260.1	55%	-	87
hy		hydratase [Homo sapiens]		%69	363	401
blastx.2 G		GLUCOSAMINE	sp O94808 GFA2_H	100%	193	1299
<u>ri</u>		FRUCTOSE-6-	UMAN	%86	1301	1468
<u>a</u>	-	PHOSPHATE			_	
	7	AMINOTRANSFERASE				
HMMER P	15	PFAM: Glutamine	PF00310	74.1	124	348
	8	amidotransferases class-Ⅱ	-			
HIMMER I	1	PFAM: Glutamine	PF00310	92.7	3	233
2.1.1	⊒	amidotransferases class-Ⅱ				
blastx.2 GI		GLUCOSAMINE	sp 094808 GFA2_H	85%	3	995
FR	\sim	FRUCTOSE-6-	UMAN			
<u> </u>		PHOSPHATE				
<u> </u>		AMINOTRANSFERASE				
blastx.2 C		CG9630 PROTEIN.	sp Q9VHU1 Q9VHU	47%	145	774
				25%	955	1044
+	- 12			0/ 67	0//	0/1
MER	Щ.	PFAM: Helicases	PF00271 .	84.64	156	286
1.8 <u>d</u>		conserved C-terminal domain				
blastx.14 (I C	(AJ010469) RNA helicase	gi 3776011 emb CAA	54%	756	514
	.▼.	Arabidopsis thaliana]	09208.1	49%	516	310
blastx.2	Ы	PUTATIVE ATP-	sp 043630 043630	%66	1121	78

		124		530		204			893	1942	1640	1013	1063			373	622	91	1140	460	934	853	1228	179	120	233
		2		21		22		,	3	1469	1161	834	923			137	206	76	1063	413	863	737	1154	304	245	313
		7.62		%86		52.06			37%	25%	34%	40%	13.09			45%	43%	26%	20%	26%	45%	30%	44%	64%	%69	48%
		PF00271		sp[Q9UNC8 Q9UNC		PF00271			sp AAG09428 AAG0	9428			PF00271			gj 4405795 gb AAD1	9826.1							sp O60448 O60448		
DEPENDENT	MITOCHONDRIAL	PFAM: Helicases	conserved C-terminal	5	RECUS GAIMINA).	PFAM: Helicases	conserved C-terminal	domain	RNA helicase.				PFAM: Helicases	conserved C-terminal	domain	(AF038963) RNA	helicase [Homo sapiens]	1						NEURONAL THREAD	PROTEIN AD7C-NTP.	
		HMMER	1.8	blastx.2		HMMER	1.8		blastx.2				HMMER	1.8		blastx.14								blastx.2		
		741		185		742			186				743											187		_
		509775		1102698		863846			1130816				965476											1192287		
		HAGBA63		HBMUG47		HBMUG47			HCRPZ84				HCRPZ84											HCWTR54		

HCWTR54 729290 744 HW HDPBB41 1195686 188 blaz HDPBB41 925800 745 HW HEOPI32 907903 189 HW				27%	331	233
1 729290 744 1 1195686 188 1 925800 745 907903 189 1151479 190 960973 746 1182719 191 1182719 191 1182719 191				85%	364	344
1195686 188 1 925800 745 907903 189 1151479 190 960973 746 1182719 191 1182719 191	HMMER	PFAM: Helicases	PF00271	6.14	151	198
1195686 188 1 925800 745 907903 189 1151479 190 960973 746 1182719 191 1182719 191	1.8	conserved C-terminal domain				
1 925800 745 907903 189 1151479 190 960973 746 1182719 191	blastx.2	RNA helicase HEL117 -	pir A57514 A57514	%06	2411	564
1 925800 745 907903 189 1151479 190 960973 746 1182719 191 1 908374 747		rat		%88	2722	2372
1 925800 745 907903 189 1151479 190 960973 746 1182719 191				45%	2814	2545
907903 189 1151479 190 960973 746 1182719 191 1 908374 747	HMMER	PFAM: Helicases	PF00271	108.7	47	292
907903 189 1151479 190 960973 746 1182719 191 1 908374 747	2.1.1	conserved C-terminal				
907903 189 1151479 190 960973 746 1182719 191 1 908374 747		domain				
907903 189 1151479 190 960973 746 1182719 191 1 908374 747	blastx.14	(AF106680) RNA	gi 5410326 gb AAD4	82%	17	637
907903 189 1151479 190 960973 746 1182719 191 1 182719 191		helicase [Hómo sapiens]	3033.1			
1151479 190 960973 746 1182719 191 1 908374 747	HMMER	PFAM: Helicases	PF00271	89.44	176	430
1151479 190 960973 746 1182719 191 1 908374 747	1.8	conserved C-terminal		-		
1151479 190 960973 746 1182719 191 4 908374 747		domain		-		
1151479 190 960973 746 1182719 191 1 908374 747	blastx.2	DJ620E11.1A (NOVEL	sp Q9UJF0 Q9UJF0	%28	2	661
1151479 190 960973 746 1182719 191 1 908374 747		HELICASE C-				
1151479 190 960973 746 1182719 191 4 908374 747		TERMINAL DOMAIN				
1151479 190 960973 746 1182719 191 4 908374 747		AND SNF2 1 1				
960973 746 1182719 191 4 908374 747	blastx.2	PRO0478.	sp Q9UI59 Q9UI59	%19	296	1086
1182719 191 4 908374 747	HMMER	PFAM: Helicases	PF00271	6:39	454	365
1182719 191 4 908374 747	1.8	conserved C-terminal				-
1182719 191 4 908374 747		domain				
908374 747	blastx.2	probable ATP-dependent	pir E64816 E64816	81%	12	674
908374 747		RNA helicase rhlE -				
908374 747		Escherichia coli				
	HMMER	PFAM: Helicases	PF00271	128.5	151	396
2.1	2.1.1	conserved C-terminal				,
		domain				

543 664	!	470		881	207	 68	1	341		243			351		551	170			563			1606	824	389
1 644		216		210	37	2	- -	7		13			4	,	m	3		,	m			833	333	54
94%		88.81		%86	78%	48%		47%		61.91			24%		%68	10.61			24%			28%	31%	33%
gi 4062355 dbj BAA3 5457.1		PF00271		sp Q9UJF0 Q9UJF0				pir[T19508 T19508		PF00271			gi 3002558 gb AAC0	8741.1	sp CAC03449 CAC0 3449	PF00271			gb AAC36188.1			splAAG09428 AAG0	9428	
Putative ATP-dependent RNA helicase RhIE		PFAM: Helicases conserved C-terminal	domain	DJ620E11.1A (NOVEL	HELICASE C-	TERMINAL DOMAIN	AND SNF2 1 1	hypothetical protein	elegans	PFAM: Helicases	conserved C-terminal	domain	(AF026032) ATRX	protein [Mus musculus]	DJ616B8.1 (RNA HEI ICASE) (Fragment)	PFAM: Helicases	conserved C-terminal	domain	(AC005314) putative pre-	mRNA splicing factor	KNA helicase	PMA helicase		
blastx.14	-	HMMER 1.8		blastx.2				blastx.2		HMMER	1.8		blastx.14		blastx.2	HMMER	1.8		blastx.2			blocky 2	7.V190	
<u> </u>		192		•				193		748					194	749	:					105	CC1	
		907938						1106390		907951					1195070	869621	; ; ; ; ;					11/00/40	1102049	
		HFXHJ89						HHPTC55		HHPTC55					HJBBP54	HIRBD44						7 9 65.4 9 44.4	HKAHB30	

986 669		84 725	288 374			177 725			1 987		349 459			934 2001	18 923	48 152	274 345			46 333	•			22 54	·	1045 1992
	<u> </u>				!				,0																	
63.37		83%	6.01			94%			%68		17.95			%76	91%	40%	6.41			33%				9.2		%66
PF00271	,	sp CAB94754 CAB9 4754	PF00271			gb AAF34824.1 AF2	09192_1		sp BAA90955 BAA9	0955	PF00271			sp BAA97048 BAA9	7048		PF00271			gi 3876099 emb CAA	99830.1			PF00271		sp AAF82262 AAF82
PFAM: Helicases	conserved C-terminal domain	APOBEC-1 stimulating protein.	PFAM: Helicases	conserved C-terminal	domain	(AF209192) Apobec-1	complementation factor	Homo 1	CDNA FLJ20110 FIS,	CLONE COL05103.	PFAM: Helicases	conserved C-terminal	domain	Cytoplasmic dynein heavy	chain.		PFAM: Helicases	conserved C-terminal	domain	similar to dynein heavy	chain; cDNA EST	EMBL:D27549 1	[Caenorhabditis elegans]	PFAM: Helicases	conserved C-terminal	Proliferation-associated
HIMMER	1.8	blastx.2	HMMER	1.8		blastx.2			blastx.2	-	HMMER	1.8		blastx.2			HMMER	1.8		blastx.14				HMMER	1.8	blastx.2
750		196	751						197		752			198			753							754		200
862598		1151490	831356				_		1165318		856630		:	1199546			952794							926260		1222600
HKAHB56		HLDCI35	HLDCI35						HMCBU79		HMCBU79			HNTRV07			HNTRV07	,						HODEX10		HOGA010

				SNF2-like protein.	262	94%	86	1051
HOGAQ10	907911	755	HIMMER	PFAM: Helicases	PF00271	47.76	80	178
			1.8	conserved C-terminal				
				domain				
			blastx.14	lymphocyte specific	gi 805296 gb AAB08	93%	80	556
				helicase [Mus musculus]	015.1	83%	18	71
HOSBW20	982028	201	blastx.2	CG7972 PROTEIN.	sp Q9VSE2 Q9VSE2	47%	4	777
HOSBW20	668774	756	HIMMER	PFAM: Helicases	PF00271	13.94	58	96
			1.8	conserved C-terminal				
				domain				
HRADL60	1151310	202	blastx.2	probable pre-mRNA	pir T37496 T37496	40%	2750	1416
				splicing factor ATP-		42%	2750	1737
				dependent RNA helicase -				
	_			fission yeast				
				(Schizosaccharomyces				
				pombe)				
HRADL60	815196	757	HMMER	PFAM: Helicases	PF00271	14.84	248	496
			1.8	conserved C-terminal				
				domain				
			blastx.2	(AL009197) putative pre-	emb CAA15715.1	40%	83	1429
				mRNA splicing factor		44%	83	1096
				ATP-dependent RNA				
				helicase				
				[Schizosaccharomyces				•
				pombe]				
HSGSC29	1150837	203	blastx.2	ACTIN INTERACTING	sp O23240 O23240	%95	334	750
				PROTEIN.				
HSGSC29	953599	758	HMMER	PFAM: Helicases	PF00271	9.31	345	446
			1.8	conserved C-terminal		-		
				domain				

740	1494	176			1436		405	52			190	319	265	1186	3	491		3	509	1019	656	857		370			439
468	55	3			m			5			2	242	188	203		240		1	9	906	540	39		158			23
53%	%06	70.92			%06		100%	14.92			73%	84%	65%	40%		53.97			20%	39%	33%	39%		104.65			45%
gi 4006920 emb CAB	sn O9V659 O9V659	PF00271			gi 5359631 gb AAD4	2744.1 AF106019_1	sp AAF72705 AAF72 705	PF00271		,	gi 806464 gb AAB33	364.1	-	875Y69 Q9Y5L9		PF00271			gi 5106572 gb AAD3	9760.1 AF143946_1	-	sp Q9SHB9 Q9SHB9		PF00271			gi[4895231]gb AAD3
F	NEAD BOY PROTHIN		conserved C-terminal	domain	(AF106019) DEAD-box	protein [Homo sapiens]	VASA protein.	PFAM: Helicases	conserved C-terminal	domain	vasa-like gene protein,	RVI.G protein=putative	DEAD 1 [Rattus sp.]	TRANSCRIPTIONAL	ACTIVATOR SRCAP.	PFAM: Helicases	conserved C-terminal	domain	(AF143946)	transcriptional activator	SRCAP [Homo sapiens]	ATP-DEPENDENT RNA	HELICASE.	PFAM: Helicases	conserved C-terminal	domain	(AC007660) putative
blastx.14	C 110011	HMMER	1.8		blastx.14	-	blastx.2	HMMER	1.8		blastx 14			blastx.2		HMMER	1.8		blastx.14			blastx.2		HMMER	1.8		blastx.14
	200	759					205	760						206	_,	761						207		762			
	110000	920697					1102531	908360						1150877		955814						1193057		908347			
	0028	HIEDX38 HTFDX38					HTEJE15	HTEJE15						HTOES03		HTOES03						HTOHS18		HTOHS18			

[Arabidopsis thaliana]	_
T. A. N. K. TI ali access	
FFAM: nelicases	_
conserved C-terminal	0
PUTATIVE SNF2/SWI2	
FAMILY	
TRANSCRIPTION	
FACTOR.	14
CDNA FLJ20421 FIS,	\sim
CLONE KAT02467.	$\mathbf{\mathcal{C}}$
PFAM: Inositol	
monophosphatase family	\vdash
(AL032655) predicted	
using Genefinder; similar	
to I this gene	
Caenorhabditis elegans]	
BISPHOSPHATE 3'-	
NUCLEOTIDASE.	
PFAM: Inositol	
monophosphatase family	\vdash
(AF125042) bisphosphate	
o-increoudase promo sapiens]	
CDNA FLJ11068 FIS,	
CLONE PLACE1004918,	
WEAKLY SIMILAK 10 1	
PFAM: L-lactate	4-
dehydrogenases	_

															т					\neg
6901	298	523	371	1/6	558	528	100	505		535		574	275	95	330	1937			572	
53	38	218	200	777	25 540	139	ľ	520	750	305		266	84	12	277	186			258	
93%	144.25	%89	202	0.00	99%	125.4		~%88 %65	9270	123.9	1000	%08	100%	95%	%99	%86		,	243.6	
sp BAA91985 BAA9 1985	PF00056	sp Q9XT87 Q9XT87		PF00056	sp O95991 O95991	PF00151		gb AAC99994.1		DE00151	rroulli	sp 095991 095991				pir A39503 A39503			PF00390	
CDNA FLJ11068 FIS, CLONE PLACE1004918, WEAKLY SIMILAR TO	PFAM: L-lactate	LACTATE	(EC 1.1.1.27).	PFAM: lactate/malate	NMD PROTEIN.	PFAM: Lipase		similar to the following	EST sequences: GenBank	Consider a moreovery	PFAM: Lipase	NMD PROTEIN.				malate dehydrogenase	(NAD+) (EC 1.1.1)	precursor, mitochondrial -	PFAM: Malic enzyme	
blastx.2	HMMER	1.8 blastx.2	48	HMMER	blastx.2	HMMER	2.1.1	blastx.2		4000	HMMEK	blacty 2	Olement .			blastx.2			HMMER	2.1.1
212	992	213		191	214	892				,	215					216			769	
1191756	875830	1102680		526687	1228235	937999					936262					1204324			963126	1
HOENY85	HOENY85	HTEHI14		HTEHI14	HETDT70	HETDT70	0117111				HPIAT34					HDPPO41			HDPPO41	

Homo sapiens]
malate dehydrogenase (NAD+) (EC 1.1.1) precursor, mitochondrial -
human
PFAM: Malic enzyme
mitochondrial NAD/P)+
[Homo sapiens]
PFAM: Malic enzyme
malate dehydrogenase
precursor, mitochondrial human
PFAM: Fibrillar collagen C-terminal domain
collagen [Homo sapiens]
myosin heavy chain

		⊢—		ATM2 - Arabidopsis		32%	1263	1484
911341 772 HMMFR PFAM	HWMER	\dashv	PFAM	thallana (tragment) PFAM: Myosin head	PE00063	010	20	070
1.8	1.8		(motor	(motor domain) (contains ATP/GTP binding P-loop)		10:10	67	007
blastx.14 myr 61	-	-	myr 61	myr 6 myosin heavy chain	gi 1575333 gb AAB3	46%	41	274
Rattu	Rattu	Raffu	Rattu	Rattus norvegicus]	8840.1	40%	617	742
						40%	809	269
						32%	449	559
1011928	blastx.2		MYC	MYOSIN I.	sp Q63357 Q63357	93%	1	786
						100%	788	817
923702 773 HMMER PFAN 2.1.1 (moto	HIMMER 2.1.1	ER 	PFAM (moto	PFAM: Myosin head (motor domain)	PF00063	256.3	∞	640
blastx.14 myosi	-	-	myosi	myosin I [Rattus	gi 3724141 emb CAA	%16	111	640
norvegicus]	norveg	norveg	norveg	icus]	50871.1	100%	889	717
		-				100%	662	9/9
						100%	719	736
7	blastx.2		MYOS	IN I.	sp Q63357 Q63357	27%	216	3263
911447 774 HMMER PFAM 2.1.1 (motor	HMMER 2.1.1	ER	PFAM (motor	PFAM: Myosin head (motor domain)	PF00063	241.2	25	597
blastx.14 myosi			myosi norve	myosin I [Rattus norvegicus]	gi 3724141 emb CAA 50871.1	%19	-	645
685902 222 HMMER PFAN	HMMER	 	PFA	PFAM: Myosin head	PF00063	94.31	85	243
1.8 (motor ATP/C			(motor	(motor domain) (contains ATP/GTP binding P-loop)				
blastx.2 MYOSIN II			MYO	SINII	sp Q91300 Q91300	95%	85	246
INUN	(FRA	(FRA	FRA E	NONMUSCLE (FRAGMENT).				
965414 223 HMMER PFAN 2.1.1 (moto	HMMER 2.1.1	Æ	PFAI (mote	PFAM: Myosin head (motor domain)	PF00063	116.7	101	292
	-	-						

			blastx.2	myosin I gamma, MMI	pir C45438 C45438	46%	101	337
				gamma - mouse (fragment)				
HUJCL61	1223496	224	blastx.2	MYOSIN I.	sp Q63357 Q63357	%65	159	2717
						47%	2698	3207
						41%	364	414
HUJCL61	911432	9//	HMMER	PFAM: Myosin head	PF00063	196	170	544
			hlasty 14	myosin I Rattus	oil37241411emhlCAA	%CL	140	532
				norvegicus	50871.11	55%	604	750
				3	-	81%	534	599
HWLRC68	1089187	225	blastx.2	Myosin X (Fragment).	sp AAF36524 AAF36	100%	06	1238
					524	92%	1238	1276
						%99	1267	1302
HWLRC68	911481	117	HMMER 2.1.1	PFAM: Myosin head (motor domain)	PF00063	7.79	222	485
HFXFH42	713795	778	HMMER 1.8	PFAM: Neuraminidases	PF00064	9.26	259	354
HEQAN73	958912	227	HMMER 2.1.1	PFAM: Phosphoglycerate mutase family	PF00300	64.2	87	359
			blastx.2	Hypothetical 30.1 kDa protein.	sp CAC01127 CAC0 1127	%66	69	878
HSLFS31	1106294	228	blastx.2	right oriC-binding protein - Escherichia coli	pir JU0158 JU0158	%66	999	252
HSLFS31	921511	179	HMMER 2.1.1	PFAM: Phosphoglycerate mutase family	PF00300	71.6	12	149
			blastx.14	Kenn Rudd identifies as gpmB [Escherichia coli]	gi 537235 gb AAA97 291.1	96%	3	188
HELGK56	1103702	229	blastx.2	pyruvate kinase (EC 2.7.1.40) A - Escherichia	pir S29790 S29790	%96 96%	572 619	96 554

				coli				
HELGK56	925698	780	HMMER 2.1.1	PFAM: Pyruvate kinase	PF00224	406.9	147	731
			blastx.14	pyruvate kinase type II Fischerichia colil	gi 147459 gb AAA24 473.1	%86	147	731
HAMFW05	957586	230	HMMER 1.8	PFAM: Prolyl oligoneptidase family	PF00326	33.83		174
	,		blastx.2	R26984_1 (FRAGMENT).	sp 075273 075273	%56	1	558
HTEDG81	1193054	231	blastx.2	ALPHA 4 SUBUNIT OF 20S PROTEASOME.	sp Q9PTW9 Q9PTW 9	%68	79	771
HTEDG81	772995	781	HMMER 2.1.1	PFAM: Proteasome A-type and B-type	PF00227	114.6	180	488
HAMG024	943287	232	HMMER 2.1.1	PFAM: Ribonucleotide reductases	PF00268	316.2	2	490
			blastx.2	hypothetical protein DKFZp761B1312.1 - human (fragment)	pir T46249 T46249	%06	2	550
HMWBH91	1193044	233	blastx.2	house-keeping protein - mouse	pir S27870 S27870	53% 52%	282	1295 279
HMWBH91	882083	782	HMMER 1.8	PFAM: Ribosomal RNA adenine dimethylases	PF00398	23.82	385	921
HOECH19	965639	234	HMMER 1.8	PFAM: Ribosomal RNA adenine dimethylases	PF00398	116.68	173	934
			blastx.2	CGI-75 PROTEIN.	sp Q9Y384 Q9Y384	95%	140	853
						100%	911	934
HSRAA80	1121919	235	blastx.2	POLYMERASE (FRAGMENT).	sp Q9UQG0 Q9UQG 0	63%	17	361
HSRAA80	937640	783	HMMER	PFAM: Reverse	PF00078	20.88	11	130

			1.8	transcriptase (RNA-				
				dependent DNA				,
				polymerase)				
			blastx.14	(AF080232) polymerase	gj 3600069 gb AAC6	%59	17	325
				[Human endogenous	3292.1			
				refrovirus K.]				
HHEDF50	1174682	236	blastx.2	nitrogen regulation protein	pir A30377 RGECGL	%68	44	490
				II (EC 2.7.3) ntrB -		_		
		!		Escherichia coli			-	
HHEDF50	974396	784	HMMER	PFAM: Signal C termial	PF00512	115.35	65	490
			1.8	domain				•
			blastx.14	NR(II) (glnL gene	gi 41564 emb CAA28	100%	98	427
				product) (AA 1-349)	807.1			
				[Escherichia coli]	:			
HHEMK34	974395	237	HMMER	PFAM: Signal C termial	PF00512	62.83	99	277
			1.8	domain				
			blastx.2	nitrogen regulation protein	pir A30377 RGECGL	%8 <i>L</i>	20	415
				II (EC 2.7.3) ntrB -				
				Escherichia coli				
HMAGK69	1105451	238	blastx.2	hypothetical 60.6 kD	pir D65222 D65222	%96	523	26
				protein in dcub-lysu		100%	618	523
				intergenic region -		-		
				Escherichia coli (strain K-				
				12)			_	
HMAGK69	723186	785	HIMIMER	PFAM: Signal C termial	PF00512	40.87	31	405
			1.8	domain				
HNGNW52	1132300	239	blastx.2	protein-histidine kinase	pir G64840 G64840	93%	939	55
				(EC 2.7.3) - Escherichia		80%	98	42
				coli		%06	37	5
HNGNW52	883074	786	HIMMER	PFAM: Signal C termial	PF00512	174.7	464	766
							-	

			1.8	domain				
H6EDK67	974775	240	HMMER 2.1.1	PFAM: Signal peptidase I	PF00461	218.3	165	641
			blastx.2	signal peptidase (EC 3.4.99) 21K chain - dog	pir A34229 A34229	%86	93	899
HWBCS43	1151532	241	blastx.2	signal peptidase (EC 3.4.99) 18K chain - dog	pir A35309 A35309	93%	344	880
HWBCS43	772564	787	HMMER 2.1.1	PFAM: Signal peptidase I	PF00461	117.2	381	653
НСЕЗН71	189196	242	HMMER 2.1.1	PFAM: Sushi domain (SCR repeat)	PF00084	79.2	317	496
			blastx.2	seizure-related protein	pir 52657 52657	83%	5	685
				SEZ-6 precursor - mouse		64%	565	957
						30%	86	496
						48%	929	1000
HOFMS43	947973	243	HMMER 2.1.1	PFAM: Sushi domain (SCR repeat)	PF00084	. 64	174	302
		<u> </u>	blastx.2	PORCINE MEMBRANE COFACTOR PROTEIN.	sp O02839 O02839	47%	12	317
HOVCO14	947999	244	HMMER 2.1.1	PFAM: Sushi domain (SCR repeat)	PF00084	84	21	170
			blastx.2	UNKNOWN PROTEIN	sp[Q28797]Q28797	33%	21	347
				(FRAGMENT).		34%	21	380
	_					38%	424	516
						47%	424	474
HTOBE75	1161571	245	blastx.2	P-SELECTIN	sp/P16109 LEM3_H	%56	3	1067
				PRECURSOR	UMAN	38%	3	878
				(GRANULE		37%	3	998
				MEMBRANE PROTEIN		35%	3	863
				140) 1-MOLECULE 3)		34%	33	998

				(LECAM3).		39%	48	998
HTOBE75	591896	788	HMMER 2.1.1	PFAM: Sushi domain (SCR repeat)	PF00084	61.2	100	273
HCMSL08	898203	246	HMMER 2.1.1	PFAM: Calsequestrin	PF01216	1001.1	52	1221
			blastx.2	calsequestrin precursor, fast skeletal muscle - human	pir A60424 A60424	95%	112	1197
HCMSL08	959176	789	HMMER 2.1.1	PFAM: Calsequestrin	PF01216	697.4	1372	569
			blastx.14	calmitine; calsequestrine [Homo sapiens]	gij688292 gb AAB32 063.1	93%	1372	593
HDPBS64	846624	247	HMMER 1.8	PFAM: Thioredoxins	PF00085	116.87	173	493
			blastx.2	ZK973.11 protein.	sp[AAF40013]AAF40 013	32%	182	652
HDTBR50	846630	248	HMMER 1.8	PFAM: Thioredoxins	PF00085	29.85	163	297
			blastx.2	NM23-H8.	sp AAF20909 AAF20 909	100%	, 130	327
HTDAB17	890384	249	HMMER 2.1.1	PFAM: Thioredoxin	PF00085	107.9	276	533
			blastx.2	CG1837 PROTEIN.	sp Q9VYV3 Q9VYV	42%	225	518
					n	43%	231	539
HABAE22	1227053	250	blastx.2	CARBOXY TERMINUS OF HSP70-	sp Q9UNE7 Q9UNE7	%56	169	1023
				INTERACTING PROTEIN.				
HABAE22	965314	190	HMMER	PFAM: TPR Domain	PF00515	38.4	300	383

PCT/US01/01239

			2.1.1		-			
			blastx.14	(AF039689) antigen NY-CO-7 [Homo sapiens]	gi 3170178 gb AAC1 8038.1	92%	171	725
HE9MI70	1217048	251	blastx.2	UBIQUITIN CARBOXYL-	sp[P57080]UBPP_M OUSE	52%	15	758
				TERMINAL HYDROLASE 25 (EC				_
				3.1.2.15) 1 PROTEASE				
				(DEUBIQUITINATING ENZYME 25).		a		
HE9MI70	953319	791	HMMER 1.8	PFAM: TPR Domain	PF00515	16.42	154	240
HHFDK15	854734	792	HMMER 2.1.1	PFAM: TPR Domain	PF00515	21.7	213	299
HOSNZ11	1162664	253	blastx.2	conserved hypothetical protein MTH68 - Methanobacterium 1	pir E69190 E69190	36%	134	448
HOSNZ11	965875	793	HMMER 2.1.1	PFAM: TPR Domain	PF00515	30.3	144	230
			blastx.14	(AE000798) O-linked	gi 2621106 gb AAB8	34%	249	362
				GlcNAc transferase	4576.1	23%	3	236
:				[Methanobacterium thermoautotrophicum]		36%	395	484
HTAEW05	1151514	254	blastx.2	DI979N1.1 (DI979N1.1).	sp Q9UGR2 Q9UGR 2	100%	215	658
HTAEW05	838562	794	HMMER 1.8	PFAM: TPR Domain	PF00515	16.51	460	546
HTTKN45	1181807	255	blastx.2	BCDNA:GH04929 PROTEIN.	sp[Q9V3G6 Q9V3G6	23%	420	1583

HTTKN45	914589	795	HMMER 1.8	PFAM: TPR Domain	PF00515	18.74	383	469
			blastx.14	(AF181631)	gi 5901818 gb AAD5	46%	539	685
,				BcDNA.GH04929 [Drosophila melanogaster]	5417.1 AF181631_1	79%	386	487
HUSJN62	923146	256	HMMER 2.1.1	PFAM: TPR Domain	PF00515	38.4	1075	992
			blastx.2	CARBOXY TERMINUS	sp Q9UNE7 Q9UNE7	94%	1189	353
-				OF ESF /U- INTERACTING		,		
				PROTEIN.				
HTEIU92	1102681	257	blastx.2	Transketolase (EC	sp AAF76194 AAF76	71%	1	564
HTEIU92	870652	962	HMMER 2.1.1	PFAM: Transketolase	PF00456	70.1	1	225
HAQMD86	1105267	258	blastx.2	UBIQUITIN	sp O14694 UBPA H	%96	13	1878
				CARBOXYL-	UMAN		;)
				TERMINAL				
				HYDROLASE 10 (EC				
				3.1.2.15) 1 1	•			
HAQMD86	961459	161	HIMIMER	PFAM: Ubiquitin	PF00443	89.1	1700	1900
			2.1.1	carboxyl-terminal		• • • • • •		
				hydrolase family 2				
			blastx.14	similar to ubiquitin-	gi 1136438 dbj BAA1	%96	2	1879
				specific proteinase of	1507.1			
				S.cerevisiae. [Homo				
				sapiens]			•	
HBJJG02	1151462	259	blastx.2	CG5794 PROTEIN.	sp Q9VC56 Q9VC56	48%	795	1409
HBJJG02	919508	862	HMMER	PFAM: Ubiquitin	PF00443	9.08	176	460
			2.1.1	carboxyl-terminal				

				hydrolase family 2				
			blastx.14	ubiquitin hydrolase	gi 1666075 emb CAA	999	164	253
				[Homo sapiens]	66942.1	26%	314	481
						25%	20	103
						25%	485	613
						25%	979	709
						46%	281	319
						31%	821	988
						22%	188	268
HBJJN65	1151463	260	blastx.2	UBIQUITIN	sp[P57080 UBPP_M	37%	5	541
				CARBOXYL-	OUSE	-		•
				I ENVIRAGE CE CE				
				HYDROLASE 25 (EC				
				3.1.2.15) 1 PROTEASE				
				(DEUBIQUITINATING				-
				ENZYME 25).	,			
HBJJN65	960507	799	HMMER	PFAM: Ubiquitin	PF00443	80.5	514	723
			2.1.1	carboxyl-terminal				
			!	hydrolase family 2				
			blastx.14	similar to ubiquitin	gi 3878110 cmb CAA	40%	409	588
				carboxyl-terminal	87786.1	40%	209	189
				hydrolase; 1 1 cDNA EST				
				EMBL:D64405 comes				
				from this gene; cDNA				
				EST EMBL:D68146				
HBMUJ35	1195500	261	blastx.2	UBIQUITIN	H_NABUIOSXU60 ds	%16	1982	288
				CARBOXYL-	UMAN		-	
				TERMINAL				
				HYDROLASE 23 (EC				

\Box		3.1.2.15) 1 1	0.1000			
800 HMMER 2.1.1		PFAM: Ubiquitin carboxyl-terminal hvdrolase family 2	PF00443	54.6	492	355
blastx.14	(AF17	(AF177758) ubiquitin	gi 5853113 gb AAD5	%86	627	355
	specif	specific protease 16	4321.1 AF177758_1	91%	359	288
760 bloomy	T CED	TOTAL SAPICIES	113/1100/12/13/1100/12/1	/020	1777	2000
	(FRA	-	3 Spice w 000 jes w 00 S	75%	2863	2910
801 HIMIMER	PFAIN	PFAM: Ubiquitin	PF00443	59.49	168	281
1.8	carbo	carboxyl-terminal				
	hydro]	hydrolases family 2				
263 blastx.2	UBIQ	UBIQUITIN	splQ9UK80lUBPN_H	100%	10	444
	CARE	CARBOXYL-	UMAN			
	ERM	rerminal.				
H	YDE	HYDROLASE 23 (EC			-	
3	1.2	3.1.2.15) 1 1				
802 HMMER PI	AN	PFAM: Ubiquitin	PF00443	57.8	237	377
$\begin{bmatrix} 2.1.1 & \cos \theta \end{bmatrix}$	rbo)	carboxyl-terminal				
	yaro	hydrolase family 2				
風	FAIN	PFAM: Ubiquitin	PF00443	92.4	862	1068
2.1.1	carbo? hydro]	carboxyl-terminal hydrolase family 2				•
blastx.2	EUE EUE	DEUBIQUITINATING	sp Q9UNP0 Q9UNP0	40%	409	1077
	ENZYME	YME.				
803 HMMER 211	PFAIN	PFAM: MYND finger	PF01753	33.7	393	521
\dagger	1	T CHURCH	The Constitution of the Co	, , ,		3
265 blastx.2		UBIQUITIN CARBOXYL-	splQ9Y5T3 UBPG_H UMAN	100%	7	625

				HYDROLASE 16 (EC				
	Ī			3.1.2.15) 1 1 1				
92.	924193	805	HIMMER	PFAM: Ubiquitin	PF00443	77.4	368	619
			2.1.1	carboxyl-terminal	•			
				hydrolase family 2				
			blastx.14	(AF126736) ubiquitin	gi 4454565 gb AAD2	100%	2	625
	_			processing protease	0949.1			
				[Homo sapiens]				
91	915273	908	HIMMER	PFAM: Ubiquitin	PF00443	50.1	1045	1131
			2.1.1	carboxyl-terminal	a			
				hydrolase family 2				
			blastx.14	similar to ubiquitin	gi 3879501 emb CAA	44%	889	915
				carboxyl-terminal	87795.1	28%	292	462
				hydrolase; 1 1 cDNA EST		42%	1276	1332
				EMBL:D34547 comes		35%	1093	1134
				from this gene; cDNA		23%	. 1961	2062
				EST EMBL:D37684		72%	1057	1089
99,	997643	267	blastx.2	UBIQUITIN	splP40818[UBP8_HU	82%	64	498
				CARBOXYL-	MAN	100%	1	87
				TERMINAL		79%	510	969
				HYDROLASE 8 (EC				
				3.1.2.15) 1.1				_
88	883028	807	HMMER	PFAM: Ubiquitin	PF00443	8.66	1336	1521
			2.1.1	carboxyl-terminal			_	
				hydrolase family 2			_	
115	1151518	268	blastx.2	CG3016 PROTEIN.	sp Q9W462 Q9W462	%95	361	561
						41%	16	153
917	914561	808	HMMER	PFAM: Ubiquitin	PF00443	9.69	359	568
			2.1.1	carboxyl-terminal				·
				hydrolase family 2			_	

571	129	472	480		<u>. </u>		1505	3		2239		382		<u> </u>	327	·		417		1461	 7 9		391	•		1322
473	7	368	400				1290 1			1313 2		227			28			,		0,9			2			303 13
													•													
%09	39%	37%	100%				65.2			%88		55.2			93.48			%88		350%	9/00		70.01			100%
00							-			6		-			-			_								-
SlgblAAC			W8 UBPI							084 BAA								JC5423		IB47113	21112					DOUSC 1
gi 2914695 gb AAC0	4485.1		sp Q9UMW8 UBPI HUMAN				PF00443			sp[BAA91084]BAA9	1084	PF00443			PF00201			pir JC5423 JC5423		pir/B47113/B47113			PF00201			splo9UNI6DUSC H
		la]			EC			,					<u> </u>			Ŋ. 		 	(EC	1)P-		 -
4) putativ	pecific p	sis thalia	z z	ӈ	ASE 18 (11	iquitin	rminal	amily 2	720314 F	EP07831	iquitin	rminal	amily 2	. <u>P</u> -	yl and Ul	nsferase	cylsphin	ansferase	Altransfer	7) UGT2	rabbit	P-	/l and UI	nsferases	CIFICIT
(AC003974) putative	ubiquitin specific protease	Arabidopsis thaliana	UBIQUITIN CARBOXYL-	TERMINAL	HYDROLASE 18 (EC	3.1.2.15) 1 1 1	PFAM: Ubiquitin	carboxyl-terminal	hydrolase family 2	CDNA FLJ20314 FIS,	CLONE HEP07831	PFAM: Ubiquitin	carboxyl-terminal	hydrolase family 2	PFAM: UDP-	glucoronosyl and UDP-	glucosyl transferases	2-hydroxyacylsphingosine 1-beta-	galactosyltransferase (EC	glucuronosyltransferase	(EC 2.4.1.17) UGT2B13	precursor - rabbit	PFAM: UDP-	glucoronosyl and UDP-	glucosyl transferases	DUAL SPECIFICITY
blastx.14			blastx.2	<u> </u>	<u></u>		ÆR)	HMMER 1	-	1	HMMER 1		۵			\dagger		l p	HMMER F	OI)	0.0	
blas		-	blas				HIM	2.1.1		blastx.2		H	2.1.1			1.8		blastx.2		blastx.2			H	1.8	_	blastx.2
			269	<u></u> ,			809			270		810			271					272			812			273
			1164014				862649			1223498		810403			840459					1179755			933167			981972
		17.021	HUSXU/1				X071			HWBDP39		HWBDP39			HKMMQ73					HVVBK72			HVVBK72			B52
		27.11.1	EOH —		·		HUSX071			HWB		HWB							<u>-</u>	HVVI			HVVI			H7TXB52

		378 806		1143 1292		960 1013		531 848	392 529	492 719		_	492 716	_	112 360		.25 360	467 318			515 318	_	490 1716	
		117.9			52% 10				100%	109.1				43% 3	28.6		40%	60.1			48%		100%	
UMAN		PF00782	gi 2257526 dbj BAA2	1420.1				sp AAF86649 AAF86	649	PF00782			gi 4150963 emb CAA	77232.1	PF00782		sp Q9U116 Q9U116	PF00782			gi 181840 gb AAA35	7777.1	75671417567141756	pir 114/56 114/56
PROTEIN	PHOSPHATASE 12 (EC 3.1.3.48) (EC 1	PFAM: Dual specificity phosphatase, catalytic domain	(AB004537) PROTEIN-	TYROSINE	PHOSPHATASE YVH1	[Schizosaccharomyces	pombe]	Mitogen-activated protein	kinase phosphatase x.	PFAM: Dual specificity	phosphatase, catalytic	domain	DsPTP1 protein	[Arabidopsis thaliana]	PFAM: Dual specificity	phosphatase, catalytic domain	PROTEIN PHOSPHATASE.	PFAM: Dual specificity	phosphatase, catalytic	domain	phosphatase	tyrosine/serine [Homo	sapiens)	hypothetical protein
		HMMER 2.1.1	blastx.14				_	blastx.2		HMMER	2.1.1	***	blastx.14		HIMIMER	2.1.1	blastx.2	HMMER	2.1.1		blastx.14			blastx.2
		813						274		814					275			815					750	276
		910910		-	-			1217205		971345					968763		-	971583					1,1100,	1077517
		H7TXB52				-		HDPRY71		HDPRY71					HGOCA12			HGOCA12					1	HHC129

2073	402	412	520	508	50	403	244	436	539	222	170	8/4		020	0/7	360	, 60	/77		647	 }	050	200	787	70/	478
1927	208	128	146	137	33	212	50	5	492	130	C	7		-	-		10,	101		75	2	150	2	163	701	2
75%	%09	31%	32%	27%	75%	37%	63.32	%16	%95	6.61	1000/	8/001		166.6)	83%	/8/0	07.67		20.49	÷:	54.61		%26		%88
							PF00102	gi 5817132 emb CAB	230/0.1	PF00102	pir(S40815/ATECO	Y)		PF00120		gb[AAB03004.1]	snl095833lCt 13 HTT	MAN		PF00043		PF00043		sp CAB75497 CAB7	5497	sp O88741 O88741
DKFZp564F0923.1 -	human (fragment)					DEANG P. L.	Fraux: Frotein-tyrosine phosphatase	(AL110210) hypothetical protein [Homo sanions]	DEANGE TO SEPTOND	FFAIM: Frotein-tyrosine phosphatase	glutamateammonia	ligase (EC 6.3.1.2) -	Escherichia coli	PFAM: Glutamine	synthetase	glutamine synthetase Fischerichia colil	CHLORIDE	INTRACELLULAR	CHANNEL PROTEIN 3.	PFAM: Glutathione S-	transferases.	PFAM: Glutathione S-	transferases.	t t	sed 1	GANGLIOSIDE-
						THAMED	1.8	blastx.14	משאיים	1.8	blastx.2	·		HMMER	2.1.1	blastx.2	blastx.2			HMMER	1.8	HMMER	1.8	blastx.2		blastx.2
						816	2		277	1	278			817			279			818		280				281
					-,···	916885			973449)).	1229467			576093			1121932			957854		960302				1103488
						HHCJ29			HODGC61		HBXGQ52			HBXGQ52		·	HE2JS39		TELOTOR	HEZJS39		HE/SH2]			1000	HMIA023

				INDUCED				
				DIFFERENTIATION ASSOCIATED PROTEIN				
HMIA023	675329	819	HMMER	1. PFAM: Glutathione S-	PF00043	29.5	23	184
			2.1.1	transferases.				
HELDW45	944301	282	HMMER	PFAM:	PF00408	133.1	114	512
			2.1.1	Phosphoglucomutase/phos				
				phomannomutase				
			blastx.2	phosphoglucomutase (EC	pir G64803 G64803	%66	3	512
				5.4.2.2) - Escherichia coli	. !			
HSRBB31	1121889	283	blastx.2	3-methylcrotonyl-CoA	sp BAA99407 BAA9	100%	3	440
	_			carboxylase biotin-	9407	64%	493	861
				containing 1		54%	395	526
						71%	707	790
HSRBB31	958210	820	HMMER	PFAM: Biotin-requiring	PF00364	75.97	1455	1643
			1.8	enzymes				
HTEOW39	1151517	284	blastx.2	lysozyme (EC 3.2.1.17) -	pir JE0185 JE0185	46%	. 65	484
				bare-faced crassow				
HTEOW39	870566	821	HMMER	PFAM: C-type lysozymes	PF00062	126.92	59	295
			1.8	and alpha-lactabulmin				
HE2PE32	1106571	285	blastx.2	6-phospho-beta-	pir/B65175/B65175	85%		540
				glucosidase (EC 3.2.1.86)				
				bglB - Escherichia coli				
HE2PE32	524511	822	HIMIMER	PFAM: Glycosyl	PF00232	87.26	17	289
			1.8	hydrolases family 1				
HSIDW39	1211446	286	blastx.2	Cytosolic beta-	sp CAC08178 CAC0	%66	99	748
				glucosidase (Fragment).	8178			
HSIDW39	775139	823	HMMER	PFAM: Glycosyl	PF00232	134	28	372
			2.1.1	hydrolase family 1				

			blastx.2	cytosolic beta-glucosidase [Cavia porcellus]	gb[AAB41058.1]	84%	-	363
HSIDW39	830774	824	HMMER 2.1.1	PFAM: Glycosyl hydrolase family 1	PF00232	155.5	42	419
HPMLD30	1226192	287	blastx.2	alpha-glucosidase (EC 3.2.1.20) - Escherichia coli	pir C64769 C64769	%96	44	1543
HPMLD30	937414	825	HMMER 1.8	PFAM: Alpha amylases (family of glycosyl hydrolases)	PF00128	18.21	402	479
			blastx.2	maltodextrin glucosidase [Escherichia coli]	gb AAB40159.1	%66	30	485
HOEKP17	1204712	288	blastx.2	FLAVOHEMOPROTEIN B5+B5R.	eIHU69/eIHU69/qs	%06 62%	749 214	1675 870
HOEKP17	931049	826	HMMER 2.1.1	PFAM: Heme-binding domain in cytochrome b5 and oxidoreductases	PF00173	9.69	258	428
			blastx.14	(AL032654) similar to Heme-binding domain in	gi 3881161 emb CAA 21721.1	92%	261	473
				-		%09	156	215
						20%	1253	1318
						39%	1565	1648
						21%	1352	1393
						25%	1055	1081
						45%	580	639
HFXDP67	1228141	289	blastx.2	hypothetical protein b0872 - Escherichia coli	pir H64825 H64825	95%	240	1205
HFXDP67	526951	827	HMMER 1.8	PFAM: FAD/NAD-binding domain in	PF00175	13.6	293	415

				oxidoreductases				
HJABA59	1199933	290	blastx.2	METHIONINE SYNTHASE REDUCTASE.	splQ9UBK8 Q9UBK 8	%16	2	904
HJABA59	713642	828	HMMER 1.8	PFAM: FAD/NAD- bínding domain in oxidoreductases	PF00175	100.6	423	797
HKIXB03	1129055	291	blastx.2	CYTOCHROME B5 REDUCTASE B5R.2.	sp Q9UHJ0 Q9UHJ0	93% 82% 88%	197 2 70	370 88 96
HKIXB03	924636	829	HMMER 1.8	PFAM: FAD/NAD-binding domain in oxidoreductases	PF00175	31.48	192	326
			blastx.2	(AL133582) hypothetical protein [Homo sapiens]	emb CAB63726.1	85%	144	371
HKMMF49	1124742	292	blastx.2	Kidney superoxide- producing NADPH oxidase.	sp BAA95695 BAA9 5695	100%	10	009
HKMMF49	096229	830	HMMER 2.1.1	PFAM: Ferric reductase like transmembrane component	PF01794	63.6	79	294
HLDOG51	1151491	293	blastx.2	Neurospora crassa hypothetical protein 15E6.170 - Neurospora crassa	pir T48809 T48809	40%	163	522 800
HLDOG51	918840	831	HMMER 2.1.1	PFAM: Oxidoreductase FAD/NAD-binding domain	PF00175	62.6	524	904
			blastx.14	phenolhydroxylase component [Acinetobacter	gi 535285 emb CAA8 5385.1	32%	269	370

		_		calcoaceticus		37%	647	727
						42%	527	583
						44%	215	897
HSVAI25	1130819	294	blastx.2	Hypothetical 12.9 kDa	sp/BAB12124/BAB1	58%	524	652
				protein.	2124	%99	663	761
HSVAI25	577154	832	HIMMER	PFAM: FAD/NAD-	PF00175	7.34	126	212
			1.8	binding domain in				
HSXCP56	924635	295	HMMER	PFAM: FAD/NAD-	PF00970	162.3	243	200
		v)	2.1.1	binding Cytochrome			-	
				reductase				
			blastx.2	CYTOCHROME B5	sp Q9UHJ0 Q9UHJ0	%16	171	950
				REDUCTASE B5R.2.		100%	142	240
HBCAT08	1167275	296	blastx.2	PXN PROTEIN.	sp Q9VZZ4 Q9VZZ4	46%	71	2419
						37%	2237	2461
			_			20%	3295	3351
						36%	157	246
HBCAT08	920940	833	HMMER	PFAM: Peroxidases	PF00141	32.87	3	347
			1.8	4	14 A CIL: IE JONO A D 2 11.	/800	101	247
			blastx.14	similar to D.melanogaster	gi[1504040 db] BAA1	9/76		746
•				peroxidasin(U11052)	3219.1	93%	m	134
				[Homo sapiens]		95%	160	198
						29%	133	183
HHFBU53	1048855	297	blastx.2	subtilisin-like proprotein	pir A39490 A39490	85%	4	570
				Collycliase (EC 5.4.21) DACEA precursor enlice				
				form A - human			-	
HHFBU53	837647	834	HMMER	PFAM: Proprotein	PF01483	254.1	381	797
			2.1.1	convertase P-domain				
HTTD045	942505	298	HIMMER	PFAM: Thiolase	PF00108	794.8	459	1637
		-						

			211					
			blastx.2	3-oxoacyl-CoA thiolase -	pir S43440 S43440	95%	456	1640
	!			human				
HTPII72	1104236	299	blastx.2	valinetRNA ligase (EC 6.1.1.9) - rat (fragment)	pir PN0473 PN0473	51%	4	657
HTPI172	958035	835	HMMER 1 8	PFAM: tRNA synthetases	PF00133	280.02	4	645
	·	· · · · · ·	hlacty 14	transfer RNA-Val	9120762519hIAAA42	26%	4	576
				synthetase [Rattus	320.1	51%	589	750
				norvegicus]	-	28%	780	998
H6BSE22	1151371	300	blastx.2	UBIQUITIN CARBOXYL-	sp Q9Y5T5 UBPG_H UMAN	%66	156	623
				TERMINAL				
				HYDROLASE 16 (EC				
-		_		3.1.2.15) 1 1 1				
H6BSE22	969019	836	HMMER	PFAM: Ubiquitin	PF00442	41.8	738	833
			2.1.1	carboxyl-terminal				
				hydrolases family 2				
·			blastx.14	(AF126736) ubiquitin	gi 4454565 gb AAD2	94%	672	1493
				processing protease	0949.1	100%	156	602
				[Homo sapiens]		94%	1482	1538
				1		100%	1573	1599
						42%	1452	1514
						20%	781	810
HDPAE43	1220621	301	blastx.2	Ubiquitin specific	sp AAF66953 AAF66	%08	114	1586
				protease (Fragment).	953			
HDPAE43	864998	837	HMMER	PFAM: Ubiquitin	PF00442	63.9	236	331
			2.1.1	carboxyl-terminal				
HDDFM16	1103042	302	blacty 2	CG8830 PROTFIN	spl09V6C0l09V6C0	53%	180	470
ALLOI LIMETO	7100011	305	Ottooth.		25. 22. 20. 20. 20. 20. 20. 20. 20. 20. 20			

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				20%	983	1201
		,	,	30%	1571	1828
				41%	611	778
				41%	1319	1435
ER.	YY.	PFAM: Ubiquitin	PF00442	62	163	258
2.1.1 ca hy	rbox drol	carboxyl-terminal hydrolases family 2				
303 blastx.2 C	DNA	CDNA FLJ10809 FIS,	sp[BAA91825 BAA9	%69	330	518
) ß	EA.	WEAKLY SIMILAR TO	5781			
	11	•				
839 HIMIMER	PFAM	PFAM: Ubiquitin	PF00442	32.31	417	470
1.8	carbox hydrol	carboxyl-terminal				
Ť	10 10 1		\$ 200 miles			
blastx.14 (AL03	mtm	gi 3560166 emb CAA	20%	345	464
<u> </u>	arbox	erminal	20678.1	33%	466	555
- h	drol	hydrolase				
S]	chiz	Schizosaccharomyces				
E.	pombe	[9]				
MER	PFAM	PFAM: Ubiquitin	PF00442	11.44	131	181
1.8	arbox	carboxyl-terminal				
	hydrol	hydrolases family 2				
305 blastx.2	UBIQI		sp 075317 UBPC_H	%76	162	536
	CARB	<u></u>	UMAN			
	TERM	TERMINAL		-		
	HYDR	HYDROLASE 12 (EC				
	3.1.2.1	3.1.2.15) 1 1 1	:			
841 HIMMER	PFAM	itin	PF00442	58.8	231	326
2.1.1	carbox	carboxyl-terminal				

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491	122	1859	962	2265	842	1754	955	2167	2169	577	531			223	3	523	547		957	594	603
222	06	963	246	1870	699	1596	872	626	2143	512	1			2	,	116	116		100	259	100
%98	11.1	%66	%66	%66	37%	37%	28.2	93%	100%	45%	%66	-		125.4		114.97	100%		48%	124.58	42%
sp AAF71030 AAF71 030	PF00442	sp CAB93533 CAB9	3533				PF01302	gb AAF29029.1 AF1	61542_1		pir A64874 GWEC			PF00218	TOOOOO	FF00089	sp AAF44349 AAF44	349	sp Q9UL52 Q9UL52	PF00089	gb AAF04328.1 AF0 64819_1
PRO0758.	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	Cyld protein.					PFAM: CAP-Gly domain	(AF161542) HSPC057	[Homo sapiens]		indole-3-glycerol-	phosphate synthase (EC	4.1.1.48) / 1 coli	PFAM: Indole-3-glycerol	DEAM: Transit	rraid: 11ypsin	Complement C1r-like	proteinase precursor.	SERINE PROTEASE DESC1.	PFAM: Trypsin	(AF064819) serine protease DESC1 [Homo
blastx.2	HMMER 1.8	blastx.2					HMMER 2.1.1	blastx.2			blastx.2			HMMER 7 1 1	UN O ATO	1.8	blastx.2		blastx.2	HMMER 1.8	blastx.2
306	842	307					843				308			844	300	506			310	846	
1124600	866951	1196787	-				973570				1103305	,		663955	274055	7/4022			1154961	947067	
HSATQ28	HSATQ28	HTPIL46					HTPIL46				HNGEN37			HINGEN37	TI MOO77	//Odivina			HNKAZ51	HNKAZ51	

_	171 881	165 890	1	161 871													
46%	322.84	%66	21.000	320.10	950.10	99%	99%	99% 82.96 100% 94%	99% 82.96 100% 94%	99% 82.96 100% 94% 309.92	99% 82.96 100% 100% 309.92	99% 82.96 100% 309.92 309.92	99% 82.96 100% 94% 93% 93%	99% 82.96 100% 100% 309.92 93% 93%	99% 82.96 100% 309.92 309.92 337.1	99% 82.96 100% 309.92 33% 93% 93%	99% 82.96 100% 94% 93% 93% 93%
0000000	PF00089	sp 043342 043342	PF00089		gb AAB93671.1	gb[AAB93671.1 PF00089	gb AAB93671.1 PF00089 sp Q9UI38 Q9UI38	\$b AAB93671.1 PF00089 \$p Q9UI38 Q9UI38 \$p Q9UKQ9 KLK9_	gb AAB93671.1 PF00089 sp Q9UI38 Q9UI38 sp Q9UKQ9 KLK9_ HUMAN	gb AAB93671.1 PF00089 sp Q9UI38 Q9UI38 sp Q9UKQ9 KLK9_ HUMAN PF00089	gb AAB93671.1 PF00089 sp Q9UI38 Q9UI38 sp Q9UKQ9 KLK9_ HUMAN PF00089 gb AAD26427.2 AF1 35026_1	gb AAB93671.1 PF00089 sp Q9UI38 Q9UI38 sp Q9UKQ9 KLK9_ HUMAN PF00089 gb AAD26427.2 AF1 35026_1	gb AAB93671.1 PF00089 sp Q9UI38 Q9UI38 sp Q9UKQ9 KLK9_ HUMAN PF00089 gb AAD26427.2 AF1 35026_1 PF00171	gb AAB93671.1 PF00089 sp Q9UI38 Q9UI38 sp Q9UKQ9 KLK9_ HUMAN PF00089 gb AAD26427.2 AF1 35026_1 PF00171 sp O94788 DHAS_H	gb AAB93671.1 PF00089 sp Q9UI38 Q9UI38 sp Q9UKQ9 KLK9 HUMAN PF00089 gb AAD26427.2 AF1 35026_1 PF00171 sp O94788 DHAS_H UMAN	gb AAB93671.1 PF00089 sp Q9UI38 Q9UI38 sp Q9UKQ9 KLK9_ HUMAN PF00089 gb AAD26427.2 AF1 35026_1 PF00171 sp O94788 DHAS_H UMAN	gb AAB93671.1 PF00089 sp Q9UI38 Q9UI38 sp Q9UKQ9 KLK9_ HUMAN PF00089 gb AAD26427.2 AF1 35026_1 PF00171 sp O94788 DHAS_H UMAN
sapiens	FrAM: Irypsın	SP001LA (FRAGMENT).	PFAM: Trypsin		(AC003965) SP001LA [Homo sapiens]	(AC003965) SP001LA [Homo sapiens] PFAM: Trypsin	(AC003965) SP001LA [Homo sapiens] PFAM: Trypsin TESTES-SPECIFIC PROTEIN TSP50.	ILA	FIC 0. KREIN-			C C C C C C C C C C C C C C C C C C C		C C C C C C C C C C C C C C C C C C C	A BR	A GIN-	H. B. C.
1	HIMIMEK F		HMMER P		blastx.2 (4	2		2	<u>ي</u>	W W	2 2		2 2	XX.2 WER AER AER AER	X.2 X.2 X.2 X.2 X.2 X.2 X.2 X.2	XX.2 WER AER AER ACC ACC ACC ACC ACC A	VER VER VER VEX.2 XX.2 XX.2 XX.2 XX.2 XX.2 XX.2 XX.2
1	311		5 847			5 312				_							
010000	919899		947085			957456	957456	957456	957456								
HOGDB01	HOGDROI		HOGDR01			HUKEP18	HUKEP18	HUKEP18	HUKEP18	HUKEP18 HWHGF95 HWHGF95	HUKEP18 HWHGF95 HWHGF95	HUKEP18 HWHGF95 HWHGF95	HUKEP18 HWHGF95 HWHGF95	HUKEP18 HWHGF95 HWHGF95	HUKEP18 HWHGF95 HWHGF95 HEMFC61	HUKEP18 HWHGF95 HWHGF95 HEMFC61	HUKEP18 HWHGF95 HWHGF95

			2.1.1					
·			blastx.2	beta-lactamase (EC 3.5.2.6) - phage phi-X174	pir S47061 S47061	%56	169	1026
HHEKZ12	878267	316	HMMER 1.8	PFAM: Beta-lactamases	PF00144	132.1	102	380
			blastx.2	beta-lactamase (EC 3.5.2.6) - phage phi-X174	pir S47061 S47061	%86 %86	21 377	377 436
HHELA35	878217	317	HMMER 2.1.1	PFAM: Beta-lactamase	PF00144	175.4	118	450
			blastx.2	beta-lactamase (EC 3.5.2.6) - phage phi-X174	pir S47061 S47061	%86	37	450
HSYBQ34	972295	849	HMMER 1.8	PFAM: Beta-lactamases	PF00144	387.58	2697	3473
HFCBA44	948533	319	HMMER 1.8	PFAM: Carboxylesterases	PF00135	34.24	315	485
			blastx.2	thiolesterase B (EC 3) precursor - mallard	pir A47162 A47162	56% 60% 48%	2 423 184	208 482 264
HOUBE50	948519	320	HMMER 1.8	PFAM: Carboxylesterases	PF00135	55.97	16	243
	!		blastx.2	Neuroligin 3 isoform HNL3s (Fragment).	sp AAF71231 AAF71 231	70%	31	243
HDPAS16	734057	321	HMMER 2.1.1	PFAM: Carbamoyl- phosphate synthase (CPSase)	PF00289	137.8	220	495
.,			blastx.2	3-methylcrotonyl-CoA carboxylase biotin-containing 1	sp BAA99407 BAA9 9407	%68	112	495
HFLAA23	960332	322	HMMER 2.1.1	PFAM: FGGY family of carbohydrate kinases	PF00370	314	137	784

784	872	998	300	100	0 -	٠,		0	-	9	7	وا			4		1			1			6	
		_		15	1120	+	1001	92	251	986	29	306			374		1487	?		1487				'
000	291	255	19	5	506	170	2/5	393	195	939	250				297		1128)		735			387	
86%	194.57	92%	%86	29%	94%	0/00	7:007	53%	78%	75%	37%	%68			34.8	_	60.76		-	82%			100.08	
pir S47801 S47801	PF00109	sp BAA91286 BAA9	1286		sp BAA91286 BAA9 1286	DE00100	2010011	gi 2984031 gb AAC0	7574.1[pir/H64949/H64949			PF00384		PF00361			pir C65024 C65024		-	PF00361	
L-xylulokinase (EC 2.7.1.53) - Escherichia coli	PFAM: Beta-ketoacyl synthases	CDNA FLJ20604 FIS,	CLONE KAT06449.		CDNA FLJ20604 FIS, CLONE KAT06449	PFAM: Beta-ketoacivi	synthase	(AE000752) 3-oxoacyl-	[acyl-carrier-protein]	synthase II [Aquifex	aeolicus]	biotin sulfoxide reductase	(EC 1) 2 - Escherichia	COIL	PFAM: Prokaryotic molybdopterin	oxidoreductases	PFAM: NADH-	Ubiquinone/plastoquinone	, various chains	hypothetical protein	b2484 - Escherichia coli	(strain K-12)	PFAM: NADH-	Ubiquinone/plastoquinone
blastx.2	HMMER 1.8	blastx.2			blastx.2	HWMER	2.1.1	blastx.14				blastx.2			HMMER 2.1.1		HMMER	1.8		blastx.2			HMMER	1.8
	323				324	850						325			851		326						852	
	922112				1103330	922115						1155464		1,2000	582754		891067						956591	
	HCFMZ90				HFCES27	HFCES27					The state of the s	HSDFK/8		TION	HSDFK78		HSDJX58						HSDJX58	

				suich sucher				
****				, various citatiis				
			blastx.2	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3)	dbj BAA16372.1	100%	814	1572
				chain 5 [Escherichia coli]				
HSLHV27	1105339	327	blastx.2	NADH dehydrogenase	pir D64999 D64999	93%	94	927
				(ubiquinone) (EC 1.6.5.3)				
				coli				
HSLHV27	964075	853	HMMER	PFAM: NADH-	PF00361	115.1	917	615
			2.1.1	Ubiquinone/plastoquinone				_
				(complex I), various			•	
				chains				
			blastx.2	NADH dehydrogenase L	emb CAA48371.1	%66	91	954
				subunit nuoL [Escherichia				
				colij				
HNGFU12	1128272	328	blastx.2	REVERSE	sp Q85732 Q85732	25%	109	543
				TRANSCRIPTASE (476				
				AA) (FRAGMENT).				
HNGFU12	971170	854	HIMMER	PFAM: RNase H	PF00075	55.68	102	290
			1.8					
			blastx.14	reverse transcriptase (476	gi 930259 emb CAA3	44%	96	422
				AA) [Woolly monkey	3367.1	%09		75
				sarcoma virus]		-		
HWLKA89	1105515	329	blastx.2	POL PROTEIN.	sp Q9WTK9 Q9WTK9	51%	260	186
						24%	885	577
						25%	135	
						64%	448	398
HWLKA89	735158	855	HMMER	PFAM: RNase H	PF00075	47.76	25	165
			1.8					
HLWBU48	1162653	330	blastx.2	ENDOGENOUS	sp Q15803 Q15803	84%	739	984

				RETROVIRUS HERV-		777%	673	752
				K(HIML6) PROVIRAL) >	1
		-		CLONE HML6.17 1 1				
HLWBU48	721520	856	HMMER	PFAM: Retroviral aspartyl	PF00077	64.25	14	280
			1.8	proteases				
HWWEY71	1204720	331	blastx.2	SERINE	spP34897 GLYM_H	%16	595	1623
				HYDROXYMETHYLTR	UMAN	%16	113	619
				ANSFERASE,				
				MITOCHONDRIAL				
				PRECURSOR 1 1				
HWWEY71	970546	857	HMMER	PFAM: Serine	PF00464	423.3	257	763
			2.1.1	hydroxymethyltransferase				
			blastx.14	SERINE	sp P34897 GLYM_H	%06	113	859
				HYDROXYMETHYLTR	UMAN			
				ANSFERASE,				
				MITOCHONDRIAL				
				PRECURSOR 1 (SHMT).				
HHFGD45	1151161	332	blastx.2	superoxide dismutase (EC	pir/A24141/DSECN	100%	880	290
				1.15.1.1) (Mn) sodA				-
				[validated] - Escherichia coli				
HHFGD45	584855	858	HMMER	PFAM: Iron/manganese	PF00081	111.46	133	267
			1.8	superoxide dismutases				·
HNHEB44	1161293	333	blastx.2	superoxide dismutase (EC	pir A24141 DSECN	100%	23	613
				1.15.1.1) (Mn) sodA	-			· · · · · ·
				[validated] - Escherichia		•		
				coli				
HNHEB44	683284	829	HMMER	PFAM: Iron/manganese	PF00081	100.87	31	150
			1.8	superoxide dismutases				

				(SODM)				
HMACX92	1151497	334	blastx.2	L-serine dehydratase (EC 4.2.1.13) - rat	pir S01009 DWRTT	%05	176	1132
HMACX92	922250	098	HMMER 2.1.1	PFAM: Pyridoxal- phosphate dependent	PF00291	224.5	203	1105
				enzyme				
			blastx.2	serine dehydratase (AA 1 - 327) [Rattus norvegicus]	emb CAA68721.1	61%	197	1153
HNTBW57	1193070	335	blastx.2	CDNA FLJ10916 FIS,	sp BAA91904 BAA9	%08	958	1302
				CLONE	1904	%001	613	777
				OVARC1000309, WEAKLY SIMILAR TO				
				1				
HNTBW57	867327	861	HMMER	PFAM: Serine/threonine	PF00291	41.43	425	673
			1.8	dehydratases, cysteine				
THOUSE CASE	110000	,		symmase and cystannolmie				
HBSDC13	1105677	336	blastx.2	tartronate-semialdehyde	pir JT0742 JT0742	%89	353	718
				synthase (EC 4.1.1.47) -		83%	124	423
				Escherichia coli		51%	622	066
						85%	840	959
						%96	47	130
HBSDC13	657402	862	HMMER	PFAM: Thiamine	PF00205	26.75	3	182
			1.8	pyrophosphate enzymes				
HCWBX21	920486	337	HMMER	PFAM: Thiamine	PF00205	22.15	82	261
			1.8	pyrophosphate enzymes				
			blastx.2	tartronate-semialdehyde	pir[JT0742]JT0742	%88	85	369
				synthase (EC 4.1.1.47) -		%96	8	91
				Escherichia coli		43%	374	442
HFRBW72	916944	338	HMMER	PFAM: Thiamine	PF00205	92.9	443	664
	_		2.1.1	pyrophosphate enzymes				

	-		blastx.2	pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2)	pir A23648 DEECPC	81%	407	9/9
_				- Escherichia coli				
HSLJX23	1105530	339	blastx.2	tartronate-semialdehyde synthase (EC 4.1.1.47) - Escherichia coli	pir JT0742 JT0742	%86	2	496
HSLJX23	837470	863	HMMER 1.8	PFAM: Thiamine pyrophosphate enzymes	PF00205	57.57	2	193
HSLJX90	1105297	340	blastx.2	pyruvate dehydrogenase (cytochrome) (BC 1.2.2.2) - Escherichia coli	pir A23648 DEECPC	100%	1	438
HSLJX90	787575	864	HMMER 2.1.1	PFAM: Thiamine pyrophosphate enzymes	PF00205	95.2	2	274
HAUAI67	1102604	341	blastx.2	HSPC150.	sp AAF29114 AAF29 114	100%	137	727
HAUAI67	929241	865	HMMER 1.8	PFAM: Ubiquitin- conjugating enzymes	PF00179	128.71	236	508
			blastx.14	ubiquitin-conjugating enzyme [Schizosaccharomyces pombel	gi 2330662 emb CAB 11183.1	54% 67% 32%	344 242 132	514 334 224
HDPTA89	953718	342	HMMER 1.8 blastx 2	PFAM: Ubiquitin- conjugating enzymes	PF00179	74.19	173	424
HMCBN45	927125	343	HMMER 1.8	PFAM: Ubiquitin- conjugating enzymes	PF00179	115.78	234	677
			blastx.2	hypothetical protein R09B3.4 - Caenorhabditis elegans	pir[T24069]T24069	. 53%	216	089
HTTJY18	1223495	344	blastx.2	Non-Canonical UBiquitin	sp CAB83212 CAB8	83%	376	1281

365	657		1263	526					256		469	512	86			215	}		203	340	•	560		578		1797	
330	334		292	269					20		254	468	18			42	!		9	179	-	273		270		1642	;
100%	73.94		%66	%86					150.92	•	100%	100%	30			65.1			100%	23%		80.5		85%		113.6	1
3212	PF00179		gb AAD34071.1 AF1 51834 1	pir/B65172/QQECGB					PF00483		gi 290545 gb AAA62	040.1	PF00233			PF00233			pir JE0293 JE0293			PF00481		sp Q9Z1Z6 Q9Z1Z6	•	PF00388	
Conjugating Enzyme 1 (NCUBE1).	PFAM: Ubiquitin-	conjugating enzymes	(AF151834) CGI-76 protein [Homo sapiens]	hypothetical 29.7K	protein, ibpA-gyrB	intergenic region -	Escherichia coli (strain K-	12)	PFAM: ADP-glucose	pyrophosphorylase	f270 [Escherichia coli]		PFAM: 3'5'-cyclic	nucleotide	phosphodiesterase	PFAM: 3'5'-cyclic	nucleotide	phosphodiesterase	3',5'-cyclic-nucleotide	phosphodiesterase (EC	5.1.4.1/J &B, 1	PFAM: Protein	phosphatase 2C	PROTEIN	PHOSPHATASE 2C.	PFAM:	Phosphatidylinositol-
	HMIMER 1 °	1.8	blastx.2	blastx.2					HMMER	1.8	blastx.14		HMIMER	2.1.1		HMMER	2.1.1		blastx.2			HMMER	2.1.1	blastx.2		HMMER	2.1.1
	998			345					198			,,,,	346			347						348				349	
	686056		-	1157337		_			891056			10000	558195			708888						771624				909801	
	HTTIY18			HMAJL09					HMAJL09			TIGITAGE	HSVCH3/			HTOCG37						HBXAW47				HBXAW27	

				specific phospholipase C, X domain				
			blastx.2	Phospholipase C-beta-1a.	sp CAB98142 CAB9	%16	1243	1803
HSLJE54	926924	350	HMMER	PFAM: Pyridoxal-	PF00282	35.8	342	536
			2.1.1	dependent decarboxylase				
				conserved domain				
			blastx.2	CYSTEINE SULFINIC	sindeolisindeolas	%86	198	548
				ACID		92%	542	739
				DECARBOXYLASE-		85%	721	885
				RELATED PROTEIN 4.		100%	885	806
HBXBG65	932780	351	HMMER 1.8	PFAM: Cytochrome P450	PF00067	46.55	2	535
			blastx.2	CHOLESTEROL 24- HYDROXYLASE.	sp Q9Y6A2 Q9Y6A2	%86	2	535
HE8CG83	933609	352	HMMER 2.1.1	PFAM: Protein phosphatase 2C	PF00481	42.6	757	942
			blastx.2	SCOP.	sp Q9WTR8 Q9WTR	%06	321	707
					. ∞	%01	712	1110
						%02		348
						%09	977	1021
	04					43%	41	151
						30%	118	279
						36%	369	443
HOGCW55	953161	353	HMMER	PFAM:	PF00266	56.5	132	341
			2.1.1	Aminotransferases class-V				
-			blastx.2	probable phosphoserine	pir A26998 A26998	85%	132	356
				transaminase (EC		77%	355	381
·-				2.6.1.52), progesterone-				

				induced, endometrial - rabbit				
HNTND64	954871	354	HMMER 2.1.1	PFAM: Cytochrome P450	PF00067	28.2	10	225
			blastx.2	cytochrome P450 - golden	pir 148164 148164	37%	10	264
				hamster		47%	261	329
HHAWC08	957942	355	HMMER	PFAM: IMP	PF00478	231.99	361	826
			1.8	dehydrogenase / GMP reductase				
			blastx.2	Guanosine	sp BAA93080 BAA9	%001	334	975
				monophosphate reductase	3080	100%	975	1376
				isolog.				
HFPEN04	964824	356	HMMER	PFAM:	PF00202	33.54	259	489
			1.8	Aminotransferases class-				
				III pyridoxal-phosphate				
			blastx.2	CG8745 PROTEIN.	sp Q9VU95 Q9VU95	62%	148	492
HTZMB51	496523	357	HMMER	PFAM: Lyase	PF00206	112.9	19	399
			2.1.1					
			blastx.2	adenylosuccinate lyase	pir S19212 S19212	%16	73	399
				(EC 4.3.2.2) - Escherichia		71%	2	127
LINET VA	220500	358	HAMARD	DEAM: +PNA symtheteses	DE00152	55.51	306	377
	000000	2	1.8	class II	7010011	10:00	2	4
		:	blastx.2	lysinetRNA ligase (EC	pir B65073 SYECKT	85%	58	372
				6.1.1.6) - Escherichia coli		%06	368	397
HTTDP32	558751	359	HMMER	PFAM: tRNA synthetases	PF00133	92	7	261
			2.1.1	class I (I, L, M and V)				
		_	blastx.2	PROBABLE LEUCYL-	sp Q15031 SYLM_H	%86	-	261
				TRNA SYNTHETASE,	UMAN	84%	267	365
				MITOCHONDRIAL		45%	320	424

	409	409	599	423			450	100		368)	377.	423	272		272	347		344	338		518	463
	5	14	405	241			103	7		237		231	376	189		189	267		114	75		3	341
	133.5	%96	% 96	94.5			75%	001 %001		45.8		100%	100%	33.1	-	100%	31.4		40%	118.4		77%	%76
	PF00133	pir[H64798 SYECL		PF00180			pir T13147 T13147			PF00483		sp Q9Y5P5 Q9Y5P5		PF00108		pir S43440 S43440	PF00515		sp[Q9VF81 Q9VF81	PF00328		pir B36733 B36733	
PRECURSOR 1	PFAM: tRNA synthetases class I (I, L, M and V)	leucinetRNA ligase (EC	6.1.1.4) [validated] - Escherichia coli	PFAM: Isocitrate and	isopropylmalate	uch y u og chases	180citrate dehydrogenase	beta chain isoform B -	human	PFAM: Nucleotidyl	transferase	GDP-MANNOSE	FYROPHOSPHORYLAS E A.	PFAM: Thiolase		3-oxoacyl-CoA thiolase - human	PFAM: TPR Domain		CG5038 PROTEIN.	PFAM: Histidine acid	phosphatase	acid phosphatase (EC	3.1.3.2) precursor - Fscherichia coli
	HMMER 2.1.1	blastx.2		HMMER	2.1.1	-	Dlastx.2			HMMER	2.1.1	blastx.2		HMMER	2.1.1	blastx.2	HIMMER	2.1.1	blastx.2	HIMMER	2.1.1	blastx.2	
	360	 -	-	361						362				363			364			365			
	572920			621705						715301				715860			753717			815942			
	HSLEP27			HMTAL73						НМ НВQ53				HBICG44			HSKXN70			HPIAC32		-	

WO 01/55301

HHFFP57	835955	366	HMMER	PFAM: Signal peptidase I	PF00461	32.1	218	514
			2.1.1					
			blastx.2	CG11110 PROTEIN.	656V69l959V69lqs	21%	140	574
HFKJW01	836491	367	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	174	96	440
			blastx.2	Jactaldehyde	pirlA38165[A38165	100%	96	440
		_		dehydrogenase (EC				
		_		1.2.1.22) aldA -				
				Escherichia coli		:		
HSDFL63	836498	368	HMMER	PFAM: Aldehyde	PF00171	127.4	-	234
			2.1.1	dehydrogenase family				
			blastx.2	RETINALDEHYDE-	sp 094788 DHAS_H	100%	-	249
				SPECIFIC	UMAN			
				DEHYDROGENASE				-
				TYPE 2 (EC 1.2.1)				-
				(RALDH(II)) (RALDH-				
				2).				
HLD00008	857070	369	HMMER	PFAM: Ubiquitin	PF00443	32.4	36	137
			2.1.1	carboxyl-terminal				
				hydrolase family 2				
			blastx.2	CDNA FLJ10785 FIS,	spBAA91807BAA9	100%	3	401
			_	CLONE NT2RP4000457,	1807	%08	403	220
				WEAKLY SIMILAR TO				
					,			!
HMSHN43	867363	370	HMMER	PFAM: Nucleotidyl	PF00483	53.7	70	231
			2.1.1	transferase				
			blastx.2	GDP-MANNOSE	sp Q9Y5P5 Q9Y5P5	%06	64	342
				PYROPHOSPHORYLAS				
				EA.				
HBXCT92	871044	371	HMMER	PFAM: Nucleotidyl	PF00483	49.7	105	473
	-	_						

(2) (2) (2) (3) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4				2.1.1	transferase				
Biastx	,				rigio de la companya				
St. St.				blastx.2	Eukaryotic translation	sp AAF91351 AAF91	%16	96	1451
875744 372 HMMER PFAM: Nucleotidyl PF00483 129.6 190 2.1.1 transferase blastx.2 GDP-MANINOSE sp Q9Y5P6 Q9Y5P6 99% 199 875745 373 HMMER PFAM: Nucleotidyl PF00483 89.2 261 877182 374 HMMER PFAM: Pyridine PF00070 206.97 1166 880696 375 HMMER PFAM: Ubiquitin- PF00179 69.1 85 881288 376 HMMER PFAM: Ubiquitin- PF00179 69.1 85 881288 376 HMMER PFAM: Ubiquitin- PF00443 34.2 315 881288 376 HMMER PFAM: Ubiquitin- PF00443 34.2 315 881288 376 HMMER PFAM: Ubiquitin- PF00443 315 315					subunit 3.	551			
2.1.1 transferase splQ9Y5P6 Q9Y5P6 99% 199 blastx.2 GDP-MANINOSE splQ9Y5P6 Q9Y5P6 99% 199 F. B. PYROPHOSPHORYLAS 100% 804 Blastx.2 GDP-MANINOSE splQ9Y5P6 Q9Y5P6 81% 258 Blastx.2 GDP-MANINOSE splQ9Y5P6 Q9Y5P6 81% 258 Branchedraciase B.B. PYROPHOSPHORYLAS 81% 258 Bratx.2 GDP-MANINOSE PRO0070 206.97 1166 Bratx.3 HMMER PFAMI: Pyridine PF00070 206.97 1166 Bratx.4 HMMER PFAMI: Pyridine PF00070 206.97 1166 Bratx.5 Thioredoxin reductases class-1 1325 85% 1857 1 Bratx.2 Thioredoxin reductase splAAD51325 AAD5 97% 2126 1 Bratx.2 Thioredoxin reductase splAAD51325 AAD5 98% 43 1383 1 Bratx.2 ThMMER PFAMI: Ubiquitin PF00179 96% </td <td>H6EDP44</td> <td>875744</td> <td>372</td> <td>HIMIMER</td> <td>PFAM: Nucleotidyl</td> <td>PF00483</td> <td>129.6</td> <td>190</td> <td>768</td>	H6EDP44	875744	372	HIMIMER	PFAM: Nucleotidyl	PF00483	129.6	190	768
Pigetx 2 GDP-MANNOSE SpiQ9Y5P6 Q9Y5P6 1999				2.1.1	transferase				}
PYROPHOSPHORYLAS 100% 804				blastx.2	GDP-MANNOSE	sp Q9Y5P6 Q9Y5P6	%66	199	801
Factor F					PYROPHOSPHORYLAS		100%	804	896
875745 373 HMMER PFAMI: Nucleotidyl PF00483 32% 837 2.1.1 transferase blastx.2 GDP-MANNOSE sp Q9Y5P6 Q9Y5P6 81% 258 B S77182 374 HMMER PFAMI: Pyridine PF00070 206.97 1166 B S77182 374 HMMER PFAMI: Pyridine PF00070 206.97 1166 B S77182 374 HMMER PFAMI: Pyridine PF00070 206.97 1166 B S7182 1.8 nucleotide-disulphide 97% 1226 97% 1226 B S80696 375 HMMER PFAM: Ubiquitin- PF00179 69.1 85 B S81288 376 HMMER PFAM: Ubiquitin- Sp Q9Y385 Q9Y385 96% 555 B S81288 376 HMMER PFAM: Ubiquitin- PF00443 34.2 315 B S81288 376 HMMER PFAM: Ubiquitin- PF00443 34.2 315				3	BB.		100%	65	187
8/5/45 3/3 HMMER PFAM: Nucleotidyl PF00483 89.2 261 8/7/45 2.1.1 transferase splQ9Y3F6 Q9Y5F6 81% 258 B Lastx.2 GDP-MANNOSE splQ9Y3F6 Q9Y5F6 81% 258 B TYROPHOSPHORYLAS B FRAM: Pyridine PF00070 206.97 1166 B TAMER PFAM: Pyridine PF00070 206.97 1166 B TAMER PFAM: Pyridine PF00070 206.97 1166 B SAM Diastx.2 Thioredoxin reductase class-I 1325 85% 1857 1 B SAM TR2 (Fragment). 1325 87% 1857 1 1 1383 1 B SAM TR2 (Fragment). 1.8 conjugating enzymes pF00179 69.1 85 1 B SAM TAMER PFAM: Ubiquitin PF00443 34.2 31.5 37.2 B SAM TAMER PFAM: Ubiquitin PF00443 34.2 31.5 37.2 B SAM TAMER PFAM: Ubiquitin PF00443 34.2 31.5							32%	837	938
PYROPHOSPHORYLAS Sp Q9Y5P6 Q9Y5P6 81% 258	HLJBF94	875745	373	HIMMER 2.1.1	PFAM: Nucleotidyl transferase	PF00483	89.2	261	539
PYROPHOSPHORYLAS FIGURE PRO0070 206.97 1166				blastx.2	GDP-MANNOSE	SplO9V5P6IO9V5P6	810%	250	677
877182 374 HMMER PFAM: Pyridine PF00070 206.97 1166 1.8 nucleotide-disulphide sp AAD51325 AAD5 97% 1226 blastx.2 Thioredoxin reductases class-I 1325 85% 1857 1 TR2 (Fragment). 1325 85% 1857 1 880696 375 HMMER PFAM: Ubiquitin- PF00179 69.1 85 1.8 conjugating enzymes blastx.2 CGI-76 PROTEIN. sp Q9Y385 Q9Y385 98% 43 881288 376 HMMER PFAM: Ubiquitin PF00443 34.2 315 2.1.1 carboxyl-terminal hydrolase family 2 34.2 315					PYROPHOSPHORYLAS E.B.			0	9
1.8 nucleotide-disulphide oxidoreductases class-I blastx.2 Thioredoxin reductase sp[AAD51325 AAD5 97% 1226 1857 17R2 (Fragment). 1325 85% 1857 1857 118 conjugating enzymes blastx.2 CGI-76 PROTEIN. sp Q9Y385 Q9Y385 98% 43 60% 527 11 carboxyl-terminal hydrolase family 2 1.11 carboxyl-terminal	HTEHO28	877182	374	HMMER	PFAM: Pvridine	PF00070	70 900	1166	177
Second String				1.8	nucleotide-disulphide		1	2011	<u> </u>
880696 375 HMMER PFAM: Ubiquitin PF00179 97% 1226 881288 376 HMMER PFAM: Ubiquitin PF00443 97% 43 881288 376 HMMER PFAM: Ubiquitin PF00443 98% 43 881288 376 HMMER PFAM: Ubiquitin PF00443 34.2 315 881288 376 HMMER PFAM: Ubiquitin PF00443 34.2 315					oxidoreductases class-I				
880696 375 HMMER PFAM: Ubiquitin- PF00179 69.1 85 1.8 conjugating enzymes splQ9Y385 Q9Y385 98% 43 blastx.2 CGI-76 PROTEIN. splQ9Y385 Q9Y385 98% 43 881288 376 HMMER PFAM: Ubiquitin PF00443 34.2 315 1.1.1 carboxyl-terminal hydrolase family 2 34.2 315				blastx.2	Thioredoxin reductase	sp[AAD51325]AAD5	%16	1226	432
880696 375 HMMER PFAM: Ubiquitin- PF00179 69.1 85 1.8 conjugating enzymes splQ9Y385 Q9Y385 98% 43 blastx.2 CGI-76 PROTEIN. splQ9Y385 Q9Y385 98% 43 881288 376 HMMER PFAM: Ubiquitin PF00443 34.2 315 2.1.1 carboxyl-terminal hydrolase family 2 315					TR2 (Fragment).	1325	85%	1857	1147
880696 375 HMMER PFAM: Ubiquitin- PF00179 69.1 85 1.8 conjugating enzymes sp Q9Y385 Q9Y385 98% 43 blastx.2 CGI-76 PROTEIN. sp Q9Y385 Q9Y385 98% 43 881288 376 HMMER PFAM: Ubiquitin PF00443 34.2 315 2.1.1 carboxyl-terminal hydrolase family 2 315							%16	2123	1869
880696 375 HMMER PFAM: Ubiquitin- PF00179 69.1 85 1.8 conjugating enzymes sp Q9Y385 Q9Y385 98% 43 blastx.2 CGI-76 PROTEIN. sp Q9Y385 Q9Y385 98% 43 881288 376 HMMER PFAM: Ubiquitin PF00443 34.2 315 2.1.1 carboxyl-terminal hydrolase family 2 at-2 315							41%	1383	1315
1.0 Conjugating enzymes SpiQ9Y385 Q9Y385 98% 43	HE9PC30	969088	375	HMMER	PFAM: Ubiquitin-	PF00179	69.1	85	285
881288 376 HMMER PFAM: Ubiquitin PF00443 98% 43 1 hydrolase family 2 43 43 43 43 43 43 43 43 555 43 43 555 43 557 43 527 43 527 43 527 43 527 43 527 43 527 43 527 43 527 43 527 43 527 43 527 43 527				1.0	conjugating enzymes				
881288 376 HMMER PFAM: Ubiquitin PF00443 96% 557 hydrolase family 2 hydrolase family 2 11.1 11.2				blastx.2	CGI-76 PROTEIN.	sp Q9Y385 Q9Y385	%86	43	381
881288 376 HMMER PFAM: Ubiquitin PF00443 60% 527 2.1.1 carboxyl-terminal 34.2 315 hydrolase family 2 1315							%96	555	638
881288 376 HMMER PFAM: Ubiquitin PF00443 34.2 315 2.1.1 carboxyl-terminal hydrolase family 2							%09	527	586
carboxyl-terminal hydrolase family 2	HLMDN29	881288	376	HMMER	PFAM: Ubiquitin	PF00443	34.2	315	506
hydrolase family 2				2.1.1	carboxyl-terminal				
					hydrolase family 2				

218	503	285	288	274		128	274	431	650	782	1335	1006		372	<u>.</u>	417	496	683	700		308	496	308	308
6	399	202	148	125		3	125	333	84	78	206	755		43	!	40	440	491			3	308	9	3
43%	31%	31.2	%68	53.97		%99	54%	40%	91.6	%86	%66	64%		23.8	•	100%	100%	36.5)		100%	100%	45%	43%
sp Q9V6C0 Q9V6C0		PF00063	pir A59300 A59300	PF00063		sp AAF78910 AAF78	910		PF00483	sp BAA91460 BAA9	1460			PF00483		sp Q9Y5P5 Q9Y5P5		PF00408		-	pir B64799 B64799		-	
CG8830 PROTEIN.		PFAM: Myosin head (motor domain)	myosin-If - mouse	PFAM: Myosin head	(motor domain) (contains ATP/GTP binding P-loop)	Myosin V.			PFAM: Nucleotidyl transferase	CDNA FLJ10137 FIS,	CLONE	HEMBA1003136, WEAKLY SIMILAR TO	1	PFAM: Nucleotidyl	transferase	GDP-MANNOSE	PYROPHOSPHORYLAS E A.	PFAM:	Phosphoglucomutase/phos	phomannomutase	hypothetical protein	b0644 - Escherichia coli		
blastx.2	4	HMMEK 2.1.1	blastx.2	HMMER	1.8	blastx.2			HMMER 2.1.1	blastx.2				HMMER	2.1.1	blastx.2	•	HMMER	2.1.1		blastx.2			
	100	//5		378		,			379					380				381						
	011255	(211333		911465					914401					914402				915649						
	17WD/CE70	nwbCr/8		HUKEN49			,	00000	HCUDS02					HTTJU40				HFXJX41						

308	308	562	233	281	305	496	496	457	363			375		431		373	536	534			523	856	278		275		-	
9	'n	010	717	m	30	308	308	308	10			1		363		137	363	427			20	23	3		3			
36%	30%	35%	0/00	37%	35%	39%	33%	34%	89.4			84%		43		92%	52%	48%			48.9	62%	138.5		%86			
									PF00408		,	pir G64803 G64803		PF00464		sp P34897 GLYM_H	UMAN	-			PF00089	sp O97658 O97658	PF00171		pir A38165 A38165			
	-								PFAM:	Phosphoglucomutase/phos	phomannomutase	phosphoglucomutase (EC	5.4.2.2) - Escherichia coli	PFAM: Serine	hydroxymethyltransferase	SERINE	HYDROXYMETHYLTR	ANSFERASE,	MITOCHONDRIAL	PRECURSOR 1 1	PFAM: Trypsin	SERINE PROTEASE (FRAGMENT)	PFAM: Aldehyde	dehydrogenase family	lactaldehyde	dehydrogenase (EC	1.2.1.22) aldA -	Escherichia coli
		<u>.</u>							HMMER	2.1.1		blastx.2		HIMMER	2.1.1	blastx.2	,				HMMER 2.1.1	blastx.2	HMMER	2.1.1	blastx.2			
									382					383							384		385					
									915650	>				917349							917583		918119		•			
									HSLCK91					HSLAO29							HRDBJ38		HOUES64					

HWLHU02	918520	386	HMMER	PFAM: Hexokinase	PF00349	286.7	3	395
			blastx.2	Hexokinase II.	sp CAA86476 CAA8	%6L	3	395
					6476	%99	33	395
HEAHA84	919363	387	HIMMER	PFAM: Myosin head	PF00063	36.3	87	245
			2.1.1	(motor domain)				
			blastx.2	myosin I myr 4 - rat	pir A53933 A53933	%96	87	794
						100%	794	1216
HBMXQ90	922114	388	HMMER 2.1.1	PFAM: Beta-ketoacyl synthase	PF00109	20.5	218	301
			blastx.2	CDNA FLJ20604 FIS,	sp[BAA91286[BAA9	%99	301	462
				CLONE KAT06449.	1286	%96	215	301
HOEJV72	930778	389	HMMER	PFAM: Nucleoside	PF00334	103.55	362	757
			1.8	dipnospnate kinases				
			blastx.2	NM23-H7.	sp Q9Y5B8 Q9Y5B8	%56	68	847
						29%	368	754
HRDBH58	933364	390	HIMIMER	PFAM: Aldehyde	PF00171	175.49	536	1558
			1.8	dehydrogenases				
			blastx.2	probable aldehyde	pir/H83136 H83136	767	995	1528
				dehydrogenase PA4073		34%	244	450
				[imported] - Pseudomonas			•	
				aeruginosa (strain PAO1)				
HCE3E13	951413	391	HIMMER	PFAM: tRNA synthetases	PF00133	92.6	148	603
			2.1.1	class I (I, L, M and V)				
			blastx.2	valine-tRNA ligase	pir T39630 T39630	40%	151	603
				precursor, mitochondrial -		41%	4	213
				fission yeast		44%	569	649
				(Schizosaccharomyces		83%	645	799
				μοιποεί				
HUKFO68	951652	392	HMMER	PFAM: Hexokinase	PF00349	173.1	83	340

			2.1.1					
			blastx.2	Hexokinase I (Fragment).	sp AAF28854 AAF28	16%	83	355
					854	47%	83	373
						%08	m	80
						36%	. 3	77
HFXJW08	959204	393	HMMER	PFAM: tRNA synthetases	PF00133	9.98	224	487
			2.1.1	class I (I, L, M and V)				
			blastx.2	leucinetRNA ligase (EC	pir H64798 SYECL	82%	224	929
				6.1.1.4) [validated] - Escherichia coli		100%	3	230
HBTAD04	407351	394	blastx.2	malate synthase (EC	pir/A32649 SYECM	%86	240	1
				4.1.3.2) A - Escherichia	А			
				COII				
HBTAD04	422687	898	HMMER	PFAM: Acetyltransferase	PF00583	36.5	427	161
,			2.1.1	(GNAT) family				
HE8FG51	465267	395	HMMER	PFAM: Eukaryotic	PF01287	165.7	4	258
			2.1.1	initiation factor 5A				
				hypusine (eIF-5A)				
			blastx.2	EIF-5A2.	sp[AAF98810 AAF98 810	%86	7	267
HTPDU31	503077	396	HMMER	PFAM: haloacid	PF00702	26.3	147	296
			2.1.1	dehalogenase-like				
			blastx.2	DJ37E16.5 (NOVEL	sp Q9UGY2 Q9UGY	94%	54	323
				PROTEIN SIMILAR TO	2	100%	25	72
				NITROPHENYLPHOSP		100%	323	364
				HATASES 1				
HMUBV12	549423	397	HMMER	PFAM: Hyaluronidase	PF01630	50.7	196	303
HMHBS90	574062	398	HMMER	PFAM: UBA domain	PF00627	35.6	436	543
-	-	-						

	561	59	436		436	_		173		173				422		422	640	671	348		390		192		192	264	
	58	3	284		2			39		3				222		06	416	648	166		-		70		70	196	
	61%	100%	33.72		100%			88.8		%96				164.9		%66	%86	87%	58.3		61%		33.2		75%	47%	
	sp Q9UHX4 Q9UHX	4	PF00145		sp 043669 043669			PF01179		pir/E64889/E64889				PF00648		sp AAF99682 AAF99	682		PF00632		sp BAB13352 BAB1	3352	PF00850		sp BAA91474 BAA9	1474	
	HRIHFB2157-LIKE	PROTEIN (FRAGMENT)	PFAM: C-5 cytosine-	specific DNA methylases	PUTATIVE DNA	CYTOSINE	METHYLTRANSFERAS E DNMT2.	PFAM: Copper amine	oxidase	amine oxidase (copper-	containing) (EC 1.4.3.6)	tynA precursor -	Escherichia coli	PFAM: Calpain family	cysteine protease	Calpain large polypeptide	L2.		PFAM: HECT-domain	(ubiquitin-transferase).	NEDD4-like ubiquitin	ligase 1.	PFAM: Histone	deacetylase family	CDNA FLJ10170 FIS,	CLONE	HEMBA1003690,
211	blastx.2		HIMIMER	1.8	blastx.2			HMMER	2.1.1	blastx.2				HMMER	2.1.1	blastx.2			HMMER	2.1.1	blastx.2		HIMIMER	2.1.1	blastx.2		
			399					400						401					402				403				
			575733					577384				•		592105					657367				660310				
			HLHGH34					HELHC55						HKAAZ66					HHSCN33				HNGJQ15				

	,																				
	183	486	293	344	314	448	445	147	261	243	231	243	234	344	283	22	286	358	457	108	425
	34	-	138	30	54	347	350	25	25			25		285		2	236	194	62	10	21
	53.7	84%	55.3	36%	34%	47%	43%	89.1	92%	46%	25%	44%	52%	80%.	100%	100%	47%	25.7	%29	87%	243.4
	PF01846	splQ9WVC9lQ9WV	PF01344	sp BAA91990 BAA9	1990			PF01344	sp Q9Y2X2 Q9Y2X2									PF01685	sp[Q9R111 GUAD_	MOUSE	PE00773
WEAKLY SIMILAR TO	PFAM: FF domain	HUNTINGTON YEAST PARTNER C.	PFAM: Kelch motif	CDNA FLJ11078 FIS,	CLONE PLACE1005102,	WEAKLY SIMILAR TO		PFAM: Kelch motif	LYMPHOCYTE .	ACTIVATION-	ASSOCIATED	PROTEIN.						PFAM: Chlorohydrolase	GUANINE DEAMINASE	(EC 3.5.4.3) (GUANASE) (GUANINE 1	PFAM: RNB-like proteins
	HMMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.2				HMMER 2.1.1	blastx.2									HMMER 2.1.1	blastx.2		HMMER 2.1.1
	404		405					406										407			408
	661396		670033					677036										679292		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	685897
	HDJME16		HNTNR64				-	HMICO24						··				HSIAC23			HSLFL74

1346	428	892	933	1064	513	624		581		581	279		432	444	447	545		164	275	448	266	245	406
705	Ė	434	877	066	193	190		15		21	1		, 1	166	142	495		21	3	302	m	18	272
78%	01/6	75%	94%	48%	6'98	%08		248.4		51%	180.1		62%	93.7	%56	83%		53.3	49%	%65	78%	78%	31
pir A64877 A64877	-				PF00881	pir A40360 A40360		PF00632		sp AAF36454 AAF36 454	PF01800		L065L0 L065L0 ds	PF00899	sp 095717 095717	-		PF01344	sp CAC08185 CAC0	8185			PF00583
exoribonuclease II (EC	3.1.13.1) - Escherichia	coli			PFAM: Nitroreductase family	hypothetical protein, 20K	(selD-sppA intergenic region) - Escherichia coli	PFAM: HECT-domain	(ubiquitin-transferase).	Ubiquitin-protein ligase 1.	PFAM: Sterol O-	acyltransferase	AGRP1 PROTEIN.	PFAM: ThiF family	SUMO-1-ACTIVATING	ENZYME E1 N	SUBUNIT.	PFAM: Kelch motif	Kelch related protein 1.				PFAM: Acetyltransferase (GNAT) family
blastx.2					HIMMER 2.1.1	blastx.2		HMMER	2.1.1	blastx.2	HIMMER	2.1.1	blastx.2	HMMER 2.1.1	blastx.2			HMMER 2.1.1	blastx.2				HMMER 2.1.1
					409			410			411			412				413					414
					698259			702955			705518			707183				710377					713770
					HSDJD53			HCEBF33	•		HAPQW27			HCFLZ28	-			HWCAB58					HLMMC57
											49	4						-					

_	135	432		104	285	282	577	313	349		415	424	683	740
777	55	163	163	n ·	16		308	179	179		50	62	411	294
300/	55%	101.1	95%	0/06	117.2	100%	117.2	24.9	40%		88	72%	139.4	%06
nir(S43430)S43430		PF01008	pir T08757 T08757		PF01575	pir F64889 F64889	PF01575	PF00583	pir S43430 S43430		PF00899	sp Q9VYY3 Q9VYY	PF01613	sp P75893 P75893
diamine N-	acetyltransferase (EC 2.3.1.57) - spiny mouse (Mus saxicola)	PFAM: Initiation factor 2 subunit family	probable translation initiation factor eFf-2B	delta chain - human (fragment)	PFAM: MaoC like domain	membrane protein maoC - Escherichia coli	PFAM: MaoC like domain	PFAM: Acetyltransferase (GNAT) family	diamine N-	acetyltransferase (EC 2.3.1.57) - spiny mouse (Mus saxicola)	PFAM: ThiF family	CG1749 PROTEIN.	PFAM: Flavin reductase like domain	4- HYDROXYPHENYLAC
blastx.2		HMMER 2.1.1	blastx.2		HMMER 2.1.1	blastx.2	HMMER 2.1.1	HMMER 2.1.1	blastx.2		HMMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.2
_		415			416		698	417			418		419	
		717556			722240		868063	724795			731302		739212	
		HMELH37			HNGJI55		HNGJISS	HHGDG42			HMTMF31		HSDIF59	

	320	425	445	08	323	320	320	436	320	418	1622	1622		392	245	245	242	245	245	343
	177	174	296	ω.	174	174	174	323	174	320	117	102		132	117	m	3	12	6	245
	53.8	%19	75%	100%	36%	32%	34%	28%	30%	33%	1028.4	100%		102.4	83.8	53%	41%	42%	37%	108.4
	PF01344	sp Q9Y480 Q9Y480									PF01204	pir S04782 S04782		PF01204	PF01344	pir T33222 T33222				PF01344
ETATE 3- MONOOXYGENASE (EC 1.14.13.3).	PFAM: Kelch motif	NS1-BINDING	PROTEIN.								PFAM: Trehalase	alpha, alpha-trehalase (EC	3.2.1.28) precursor, periplasmic - Escherichia coli	PFAM: Trehalase	PFAM: Kelch motif	hypothetical protein	W02G9.2 -	Caenorhabditis elegans		PFAM: Kelch motif
	HMMER 2.1.1	blastx.2									HMMER 2.1.1	blastx.2		HMMER 2.1.1	HIMMER 2.1.1	blastx.2				HIMMER 2.1.1
	420										421			870	422					423
:	751953		····								753247			879215	769102					769103
	HNDAG60										HSLDS79			HSLDS79	нғвс де 1					HRACD17

-		_	Liosty 2	Child FI 110836 FIS	sn/BA A 91845/BA A 9	94%	2	358
			7:57	CLONE NT2RP4001228.	1845	43%	2	325
	-			WEAKLY SIMILAR TO		41%	2	337
						45%	83	343
	,			-		40%	7	355
						53%	309	386
HLDQV23	788957	424	HMMER	PFAM: Glycosyl transferases	PF00535	59.7	71	364
			blastx.2	hypothetical protein F13G3.6 - Caenorhabditis	pir T20856 T20856	42%	89	376
				elegans		CO	5	163
HPHAF45	812327	425	HMMER 2.1.1	PFAM: Kelch motif	PF01344	4.88.4	77	701
			blastx.2	CDNA FLJ10262 FIS, CLONE	sp BAA91514 BAA9 1514	100%	118	384
				HEMBB1000985, WEAKLY SIMILAR TO				
HSUME31	812373	426	HMMER	PFAM: Exonuclease	PF00929	118.4	4	441
			2.1.1 blacty 2	ISG20 PROTEIN	sp[O00441 O00441	57%	1	441
HUSHB56	815819	427	HMMER	PFAM: Calpain family	PF00648	70.1	101	346
			2.1.1	cysteine protease				
			blastx.2	CALPAIN-LIKE	sp Q9WVF0 Q9WVF	87%	65	352
HTGDN81	824708	428	HMMER	PFAM: RNB-like proteins	PF00773	395.6	417	1028
			blastx.2	virulence-associated	pir S56404 S56404	97%	417	866
				protein vacB homolog - Fscherichia coli		94%		435
,				TOOTION TOO				

427		559				Ÿ	521		521	687	570	683	637	351	354	571	671	671	908	872	1063	187	572		605
35		41					198		165	511	508	624	605	13	16	299	213	3	289	195	833	47	75		78
6.99		87%	-				. 125.1		%06	49%	71%	%59	63%	143.6	72%	41%	112.1	61%	78.1	77%	71%	%68	264.5		%09
PF00535		syl09UIV5 Q9UIV5					PF01532		sp BAA91806 BAA9	1806				PF00884	pir A44475 A44475		PF00884	sp Q9VEX0 Q9VEX0	PF00627	sp Q9Y5A7 BS4_HU	MAN		PF01008		sp Q9V9X4 Q9V9X4
PFAM: Glycosyl	transferases	UDP.	GALNAC:POLYPEPTID	EN-	ACETYLGALACTOSA	MINYLTRANSFERASE.	PFAM: Glycosyl	hydrolase family 47	CDNA FLJ10783 FIS,	CLONE NT2RP4000417,	WEAKLY SIMILAR TO			PFAM: Sulfatase	N-acetylgalactosamine-4-	sulfatase (EC 3.1.6.12) precursor - cat	PFAM: Sulfatase	CG6725 PROTEIN.	PFAM: UBA domain	BS4 PROTEIN (NY-	REN-18 ANTIGEN).		PFAM: Initiation factor 2	subunit family	CG11334 PROTEIN.
HMMER	2.1.1	blastx.2					HMMER	2.1.1	blastx.2					HMMER 2.1.1	blastx.2		HMMER 2.1.1	blastx.2	HIMMER 2.1.1	blastx.2			HMMER	2.1.1	blastx.2
429		_					430			_				431			432		433				434		
836598							837698							837782			838043		848205				848318		
HSKHY26							HKACD80							HHFDK48			HE9SS77		HAPOK49				HPMGN48		

			HMIMER	PFAM: Dienelactone	PF01738	80.3	354	1001
			2.1.1	hydrolase family				
			blastx.2	Hypothetical 34.2 kDa	sp AAG12612 AAG1	31%	330	1001
				protein.	2612			
HSLDK59 85	853385	436	HMMER	PFAM: N-	PF01510	9.08	200	736
			2.1.1	acetylmuramoyl-L-alanine				-
				amidase				
_			blastx.2	hypothetical protein	pir C64825 C64825	100%	200	1009
				b0867 precursor -		78%	183	557
HMWDI41 85	854051	437	HMMER 2.1.1	PFAM: Kelch motif	PF01344	91.2	488	595
			blastx.2	CDNA FLJ20059 FIS, CLONE COL01349.	sp BAA90921 BAA9 0921	95%	2	592
HFVHU73 856	856165	438	HMMER 2.1.1	PFAM: RNB-like proteins	PF00773	62.5	9	281
			blastx.2	ribonuclease II RNB	pir T38518 T38518	45%	6	281
				family protein - fission		38%	253	360
				yeast				
				(Schizosaccharomyces pombe)				
HMUB380 858	858497	439	HMMER	PFAM: Histone	PF00850	44.9	233	430
			2.1.1	deacetylase family				
		,	blastx.2	CDNA FLJ10328 FIS,	sp BAA91545 BAA9	93%	209	490
				CLONE NT2RM2000588,	1545	%88	477	602
				WEARLY SUMILLAR TO				
HE9ML74 859	859297	440	HIMMER	PFAM: HECT-domain	PF00632	74.3	705	914
			2.1.1	(ubiquitin-transferase).				
- , ,			blastx.2	CG5604 PROTEIN.	90'IA6O 90'IA6O ds	82%	940	1269

932	350	90	240	197			346	188			290		959	267	989		403		409	531	423	381	531	366	381	363
456	3	13	7	78	,		197	12			270		270	31	589		125		20	385	283	166	166	181	166	181
40%	43%	24.3	100%	39.8			25%	40%			244.9		72%	%86	87%		25		40%	44%	94.1	44%	32%	43%	34%	36%
		PF00850	sp AAF73076 AAF73 076	PF01557			pir G83604 G83604				PF00733		pir/A36616/AJECN				PF00534		sp AAF77213 AAF77	213	PF01344	sp Q9Y2M5 Q9Y2M	2		•	
		PFAM: Histone deacetvlase family	Class I histone deacetylase.	PFAM:	Furnarylacetoacetate	(LACA) Hydrolase tallily	conserved hypothetical	protein PA0318	[imported] - Pseudomonas	aeruginosa (strain PAO1)	PFAM: Asparagine	synthase	asparagine synthase	(glutamine-hydrolyzing)	(EC 6.3.5.4) - Escherichia	coli	PFAM: Glycosyl	transferases group 1	L165.1 (Fragment).		PFAM: Kelch motif	KELCH MOTIF	CONTAINING	PROTEIN.		
		HMMER 2.1.1	blastx.2	HIMMER	2.1.1		blastx.2		_		HMMER	2.1.1	blastx.2				HIMMER	2.1.1	blastx.2	1	HMMER 2.1.1	blastx.2				
		441		442							443						444				445					
		864092		866241							866272						867195				869137					
		HLQAJ01		HSLDP32							HPMEG40						HRADE27				HTXQR10					

124	115	97	127	167	167	182	222	252	423	482	509	200	497	801	845	460	1014		1014		341		458
5	2	ς,	5	117	117	117	166	1	1	. 3	3	153	96	499	774	422	361		313		255		234
%09	29%	61%	46%	52%	47%	45%	36%	70.7	64%	73.5	39%	200.5	84%	93%	62%	92%	255	-	94%		30.3		%98
							· [PF00773	sp CAC07620 CAC0 7620	PF01593	sp CAA84671 CAA8 4671	PF01811	pir A64806 A64806				PF00850		sp AAF73076 AAF73	0/0	PF01687		sp BAA92033 BAA9 2033
								PFAM: RNB-like proteins	Sequence 8 from Patent WO9950284.	PFAM: Flavin containing amine oxidase	R13G10.2 protein.	PFAM: Transposase	H repeat-associated	protein homolog b0706 -	Escherichia coli		PFAM: Histone	deacetylase family	Class I histone	deacetylase.	PFAM: Riboflavin kinase	/ FAD synthetase	cDNA FLJ11149 FIS, CLONE PLACE1006731.
			_					HIMIMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.2		-		HMMER	2.1.1	blastx.2		HMMER	2.1.1	blastx.2
								446		447		448				•	449				450		
								871062		871156		871996					875870				876157		
								неосв27		HE8AM04		HSLHT48					HS2SH70				HAOAE45		

t 560	3 695	5 480		480		205	404	416). 657	669	4	527	452	5 614
384	78	196	482	145	m	101	6	6	46.	49	354	180	330	93
37.5	%66	100	%66	%88	25%	61%	88	38%	35.4	52% 56%	27.2	64%	37.8	56%
PF00583	pir T08699 T08699	PF00732	sp CAB75961 CAB7	5961			PF00773	sp Q9PK00 Q9PK00	PF00561	sp Q9Y369 Q9Y369	PF00535	sp BAA97985 BAA9 7985	PF00777	splQ64686 CAG7_R AT
PFAM: Acetyltransferase (GNAT) family	hypothetical protein DKFZp564C103.1 -	PFAM: GMC oxidoreductases	Choline dehydrogenase	(Fragment).	*	,	PFAM: RNB-like proteins	EXORIBONUCLEASE, VACB/RNB FAMILY.	PFAM: alpha/beta hydrolase fold	CGI-58 PROTEIN.	PFAM: Glycosyl transferases	Brain cDNA, clone MNCb-1820.	PFAM: Sialyltransferase family	ALPHA-N- ACETYLGALACTOSA MINIDE ALPHA-2,6- SIALYLTRANSFERASE
HMMER 2.1.1	blastx.2	HIMMER 2.1.1	blastx.2				HMMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.2
451		452		. —			453	<u></u>	454		455		456	
878549	<u> </u>	878791		,-			879399		879640		880328		882939	,
HELBA42		HSPBB15	-				HTAFF91		HETHB58		HGBCU40		HE9PR39	

HTEAF36	883195	872	HMMER	PFAM: DNA/RNA non-	PF01223	148.3	274	989
			2.1.1	specific endonuclease				
HTLGW66	883855	458	HIMIMER	PFAM: Histone	PF00850	48.1	264	458
			2.1.1	deacetylase family				_
			blastx.2	HISTONE	sp Q9Z2V6 HDA5_	%65	3	605
				DEACETYLASE 5	MOUSE	58%	619	1074
				(HD5) (HISTONE		41%	903	1085
				DEACETYLASE MHDA1).		54%	171	236
HPJDV95	888844	459	HMMER	PFAM: HECT-domain	PF00632	233.1	971	1906
			2.1.1	(ubiquitin-transferase).				
			blastx.2	CG4238 PROTEIN.	290A60 290A60 ds	62%	518	1906
		_				27%	6	341
HCROF75	889436	460	HIMMER	PFAM: Isochorismatase	PF00857	46.2	252	341
			2.1.1	family				
			blastx.2	hypothetical protein	pir/T21813/T21813	21%	219	467
				F35G2.2 - Caenorhabditis		48%	135	245
				elegans				
HDPAP15	909703	461	HIMMER	PFAM: Glycosyl	PF00534	138.4	503	1051
			2.1.1	transferases group 1				-
			blastx.2	BA13B9.1 (novel protein	sp CAC07999 CAC0	100%	221	1120
				similar to a 1	7999	85%	2	79
HTGDH34	913378	873	HIMMER	PFAM: Acetyltransferase	PF00583	61.6	376	708
			2.1.1	(GNAT) family				
			blastx.14	(AF085355) N-terminal	gi 5114045 gb AAD4	%98	376	765
				acetyltransferase complex	0190.1	-		
				ard1 subunit [Homo				
				sapiens]				
HPDEH29	914591	463	HMMER	PFAM: Myosin tail	PF01576	43.8	239	454
	_	_	7.1.7					

	····		blastx.2	smooth muscle myosin	nirl1657691165769	7025	19	165
				heavy chain isoform	\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	2005	517	01
				SMemb - human		38%	305	451
				(fragment)		40%	168	233
HDPVG08	914973	464	HIMMER 2.1.1	PFAM: UBA domain	PF00627	43.4	342	461
			blastx.2	CG13472 PROTEIN.	HUV9Q/WHV9QQlqs	35%	1419	1712
	·- <u>-</u>				8	27%	297	854
						25%	555	098
The state of the s		1				44%	126	212
HFXDW32	916095	465	HMMER 2.1.1	PFAM: Domain of unknown function	PF00990	70.4	494	652
			blastx.2	probable membrane	pir H64876 H64876	<i>1</i> 9%	356	730
				protein yciR - Escherichia		64%	705	875
				coli		30%	582	719
HSSCY03	916445	466	HMMER	PFAM: HECT-domain	PF00632	96.5	764	1297
		_		(condensational).				
			blastx.2	giant protein p619 -	pir S71752 S71752	37%	311	1327
O' A ANNUA ANNUA A				пишап		0/70	153	200
HFXF149	916758	467	HMMER 2.1.1	PFAM: Isochorismatase family	PF00857	08	343	588
			blastx.2	probable membrane	pir S09671 S09671	100%	304	588
			,	protein yeaC - Escherichia				
				coli				
HTLGH72	917526	468	HMMER 2.1.1	PFAM: Peptide	PF01625	353	267	746
			: i	reductase				
			blastx.2	PEPTIDE METHIONINE	801116018611168	%00	77	776
				SULFOXIDE			1	2
				REDUCTASE (EC				_
				Y			_	-

	2110	2188	891	1171	618		909	·	714		726	_			577		577			151		382	414		116		1025
	926	1232	118	935	1250		1241		82		16		_		242		2			2		2	349		555		48
	340.1	61%	39%	64%	433.7		%88		433.7		%88		. =		210.3		92%			42.9		%06	%56	-	42.6		%06
	PF00587	pir/A38867/YSHUT			PF02126	-	sp Q60866 PTER_M	OUSE	PF02126		gi 881499 gb AAA68	951.1			PF00890		pir/B64808 DEECSF			PF00445		pir JQ0777 JQ0777			PF00583		sp Q92831 Q92831
1.8.4.6).	PFAM: tRNA synthetase class II (G, H, P, S and T)	threoninetRNA ligase	(EC 6.1.1.3) - human	`	PFAM:	Phosphotriesterase family	PHOSPHOTRIESTERAS	E RELATED PROTEIN	PFAM:	Phosphotriesterase family	parathion hydrolase	(phosphotriesterase)-	related protein [Mus	musculus]	PFAM: FAD binding	domain	succinate dehydrogenase	(EC 1.3.99.1) flavoprotein	 Escherichia coli 	PFAM: Ribonuclease T2	family	Enterobacter ribonuclease	(EC 3.1.27.6) I precursor -	Escherichia coli	PFAM: Acetyltransferase	(GNAT) family	P300/CBP-
	HMMER 2.1.1	blastx.2			HMMER	2.1.1	blastx.2		HMMER	2.1.1	blastx.14				HIMMER	2.1.1	blastx.2			HMMER	2.1.1	blastx.2			HIMMER	2.1.1	blastx.2
·	469				470				874						471					472		,			473		
-	917758				918920				919863						919034					920435					921076		
****	HSUAE63				HAPTQ56	,			HAPTO56	 - -					HNFIF54					HSDFF02			-		HE8NS06		

		-		ASSOCIATED FACTOR.		%86	1060	1248
					•	100%	→	48
					-	45%	129	185
HASBA77	921365	474	blastx.2	PEPTIDE CHAIN REI EASE EACTOR 2	sp Q53915 RF2_STR	30%	51	449
				(RF-2).				
HASBA77	921366	875	HIMMER	PFAM: Peptidyl-tRNA	PF00472	26.5	295	435
			2.1.1	hydrolase domain				
			blastx.14	PrfB [Streptomyces coelicolor]	gi 1402638 dbj BAA1 3170.1	45%	247	438
HSKDP26	921831	475	HMMER	PFAM: Site-specific	PF00239	138.8	395	81
			2.1.1	recombinases				
			blastx.2	probable resolvase b1545	pir D64909 D64909	100%	395	51
				- Escherichia coli		71%	466	404
HMTAY52	921948	476	HMMER	PFAM: Flavin containing	PF01593	78.3	224	451
			2.1.1	amine oxidase				
			blastx.2	CDNA FLJ20746 FIS,	sp BAA91360 BAA9	%46	125	880
				CLONE HEP06040.	1360	81%	866	1093
						11%	883	963
						%89	975	1022
HSDJG01	922453	477	HMMER	PFAM: HECT-domain	PF00632	105.2	121	612
			2.1.1	(ubiquitin-transferase).			_	
-			blastx.2	CYCLIN-E BINDING	sp Q9UII4 Q9UII4	%06	7	789
				PROTEIN 1.		%96	2	100
HHEPF30	928000	478	HMMER	PFAM: HECT-domain	PF00632	428	1	585
			2.1.1	(ubiquitin-transferase).				
			blastx.2	ubiquitin ligase Nedd4 -	pir S70642 S70642	%56	1	588
				rat (fragment)				
HTLAB16	929948	479	HMMER	PFAM: Flavin containing	PF01593	74.7	274	918
			2.1.1	amine oxidase				

WO 01/55301 PCT/US01/01239

			blastx.2	CDNA FLJ20746 FIS.	sp[BAA91360]BAA9	49%	217	945
				CLONE HEP06040.	1360	35%	1	186
HOHCW42	930431	480	HIMMER	PFAM: HECT-domain	PF00632	236.1	2527	1634
			2.1.1	(ubiquitin-transferase).				
			blastx.2	HYPOTHETICAL 47.0	nangolenangolds	%96	2719	1634
				KDA PROTEIN	3			-
	1			(FKAGIMEINI).				
HCHNX75	931615	481	HMMER 2.1.1	PFAM: Kelch motif	PF01344	102.5	184	324
		•	blastx.2	CDNA FLJ10748 FIS,	sp BAA91787 BAA9	46%	34	714
				CLONE NT2RP3001819,	1787	27%	37	829
				WEAKLY SIMILAR TO		27%	121	999
		•				762	262	699
HBCBA92	933093	482	HMMER	PFAM: alpha/beta	PF00561	47	1141	893
			2.1.1	hydrolase fold				
			blastx.2	Hypothetical 22.5 kDa	sp CAB97209 CAB9	%86	1315	908
				protein.	7209	100%	999	592
HHFJ131	933110	483	HMMER	PFAM: tRNA synthetases	PF00579	153.7	123	512
			2.1.1	class I (W and Y)				
			blastx.2	MITOCHONDRIAL	sp Q9UGM6 Q9UG	100%	15	512
				TRYPTOPHANYL-	M6	15%	464	577
				TRNA SYNTHETASE		%89	577	609
				PRECURSOR (EC 1				
HTXNN68	933670	484	HMMER	PFAM: Glycosyl	PF01532	540.8	1	906
			2.1.1	hydrolase family 47				
			blastx.2	hypothetical protein	pir T20009 T20009	64%	1	606
-				C47E12.3 -				
	1			Caenorhabditis elegans				
HWWFW06	6 933671	485	HMMER	PFAM: Glycosyl	PF01532	159.3	78	320
			7.1.1	nymorase raining 47				

			blastx.2	hypothetical protein	pir T20009 T20009	46%	78	530
	-			C47E12.3 -				
				Caenorhabditis elegans				
HE2SY77	934771	486	HMMER	PFAM: Biotin protein ligase	PF01317	115.6	24	299
			blastx 2	hir A hifinctional protein	nirlR24029 RVFCBF	100%	2	200
				[validated] - Escherichia		100%	301	330
				coli			2)
HSHCO49	934819	487	HIMMER	PFAM: Putative	PF01255	235.8	227	992
			2.1.1	undecaprenyl diphosphate				
				synthase				
			blastx.2	CG10778 PROTEIN.	sp Q9W3M6 Q9W3 M6	49%	134	992
HMUBI13	937820	488	HMMER	PFAM:	PF01557	288.8	327	830
			2.1.1	Fumarylacetoacetate				
				(FAA) hydrolase family				
			blastx.2	Brain cDNA, clone	sp BAA95083 BAA9	87%	237	668
				MNCb-4134.	5083			
HBXGL55	938766	489	HMMER	PFAM: Kelch motif	PF01344	150.2	1248	1388
			11.1.1	CENTA ET 11 1020 ETC	0110001011		6	0,0
			Dlastx.2	CDNA FLJ110/8 FIS,	spiBAA91990BAA9	34%	849	1838
				WEAKLY SIMILAR TO	1990	34%	127	756
	i							
HAFAH26	940254	490	HMMER	PFAM: alpha/beta	PF00561	25.5	469	774
			2.1.1	hydrolase fold				
			blastx.2	BEM46 PROTEIN.	sp 076462 076462	43%	214	1050
HARMG23	942860	491	HIMMER	PFAM: tRNA synthetase	PF00587	57.9	43	507
			2.1.1	class II (G, H, P, S and T)			-	
			blastx.2	CDNA FLJ20450 FIS,	sp BAA91176 BAA9	%98	43	612

38	1003	1129	1138	1012	694	145	628	628					774	<u></u>		1050	1718	2049	0	1331	1232	7671	504
3	863	2	65	275	1143	1356	179	80					289	 }		1769	2044	2096	77	1669	1675	2	199
100%	294.3	43%	34%	39%	142.6	29%	143.2	38%					188.7			%66	%06	100%	39%	253.8	61%		209.4
1176	PF01344	mnyegevuveglgs	5		PF00899	sp Q9VYY3 Q9VYY	PF01715	pir/T38664 T38664					PF01510			pir D64825 D64825				PF01182	pir S68445 S68445		PF01182
CLONE KAT05607.	PFAM: Kelch motif	CG6224 PROTEIN.	•		PFAM: ThiF family	CG1749 PROTEIN.	PFAM: IPP transferase	trna	isopentenyltransferase -	fission yeast	(Schizosaccharomyces	pombe)	PFAM: N-	acetylmuramoyl-L-alanine	amidase	hypothetical protein	b0868 - Escherichia coli			PFAM: Glucosamine-6- phosphate isomerase	probable glucosamine-6-	phosphate isomerase (EC	PFAM: Glucosamine-6-
	HMMER 2.1.1	blastx.2			HMMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.2					HIMMER	2.1.1		blastx.2				HMMER 2.1.1	blastx.2		HMMER
	492				493	- · · · - · · · · · · · · · · · · · · ·	494			·			495							496			497
	943224			2,00,0	949245		950713						950717							951370			951371
	HOFMV44			COLOGIA	HE9CJ28		HE8AZ89						HFXKW94							HISAF41			HDPJH11

			2.1.1	phosphate isomerase				
	_		blastx.2	probable glucosamine-6-	pir S68445 S68445	84%	130	492
				phosphate isomerase (EC				
				5.3.1.10) - golden hamster		-		
HLHCP93	951372	928	HMMER	PFAM: Glucosamine-6-	PF01182	230.7	244	267
			2.1.1	phosphate isomerase				
			blastx.2	unnamed protein product	emb CAA03416.1	%08	244	669
				[unidentified]		75%	87	197
HAIBC14	951671	499	HIMIMER	PFAM: Acetyltransferase	PF00583	42.4	311	629
a			2.1.1	(GNAT) family				
			blastx.2	Separation anxiety	sp AAF34715 AAF34	71%	299	962
				protein.	715			
HKAJZ24	921676	500	HIMMER	PFAM: Glycosyl	PF00535	74	228	779
			2.1.1	transferases				
			blastx.2	GALNAC-T5	sp Q9UGK7 Q9UGK	93%	27	827
				(FRAGMENT).	7	%29	758	805
					i.e	81%	751	783
HWADY95	951731	501	HMMER	PFAM: GMC	PF00732	190.1	29	433
			2.1.1	oxidoreductases				
			blastx.2	Choline dehydrogenase	sp CAB75961 CAB7	100%	2	514
				(Fragment).	5961			
HCHAG27	952058	502	HIMIMER	PFAM: alpha/beta	PF00561	50.8	315	521
			2.1.1	hydrolase fold			,	
			blastx.2	hypothetical protein	pir T23932 T23932	42%	785	1084
			 -	R05D7.4 - Caenorhabditis		38%	237	662
				elegans				
HPCRA07	952124	503	HMMER	PFAM: Elongation factor	PF00679	50.1	66	224
			2.1.1	G C-terminus			•	
			blastx.2	US-116 KDA.	sp O08810 O08810	91%	3	407
HDMAF23	952729	504	HMMER	PFAM: Transglutaminase-	PF01841	46.6	1271	1116
-	-	-						

			2.1.1	like superfamily				
			blastx.2	PNGase (Fragment).	sp AAF74720 AAF74 720	%66	1283	219
HRGBU12	952730	505	HMMER 2.1.1	PFAM: Transglutaminase-like superfamily	PF01841	39.7	144	299
			blastx.2	PNGase (Fragment).	sp AAF74720 AAF74	%86	9	455
		_			720	53%	454	531
						62%	522	593
, HADFD82	953295	206	HIMMER 2.1.1	PFAM: Histone deacetylase family	PF00850	309.6	118	966
			blastx.2	HISTONE	sp Q9UBN7 HDA6_	52%	118	966
				DEACETYLASE 6 (HD6).	HUMAN	53%	118	984
HCGAF54	954048	507	HMMER 2.1.1	PFAM: ubiE/COQ5 methyltransferase family	PF01209	133.3	217	423
			blastx.2	CG2453 PROTEIN.	sp Q9VYF8 Q9VYF8	%59	624	1028
						64%	202	432
						25%	541	009
HSLGA19	610031	208	blastx.2	glucosyltransferase (EC	pir B42595 B42595	%96	4	285
				2.4.1) I - Escherichia	*	100%	585	998
				coli		100%	275	475
						%06	466	588
HSLGA19	955327	877	HIMMER 2.1.1	PFAM: Glycosyl transferases group 1	PF00534	177.9	1901	1392
			blastx.2	lipopolysaccharide core biosynthesis protein	gb AAA24082.1	%86	9	098
				[Escherichia coli]				
HWWCL36	955759	509	HMMER	PFAM: tRNA synthetase	PF00587	222.3	5	610
			2.1.1	class II (G, H, P, S and T)				
			blastx.2	threonine-tRNA ligase	pir A38867 YSHUT	%9 <i>L</i>	2	658

	1284	14041	1464	648	702	734	823.	970		893	1187	1249	959	677	959	1229	99	634	310	484	361	148
	1144	t t	1691	55	1	159	581	521		393	153	1187	516	48	69	75	_	762	981	1002	1002	2
	3806		94%	53.2	87%	21%	36.7	78%		162.7	%56	100%	214	39%	37%	37%	%65	9.96	27%	73%	25%	89.9
	PF01344		sp[Q9Z2X8]Q9Z2X8	PF00561	pir G64842 G64842		PF00581	pir T50634 T50634		PF01743	sp[Q9Y362 Q9Y362		PF01344	sp Q9Y2M5 Q9Y2M	2			PF01344	sp Q9Y2X2 Q9Y2X2			PF01557
(B) (113) 1	PFAM: Kelch motif		KEAP1 PROTEIN.	PFAM: alpha/beta hydrolase fold	probable hydrolase b1009	- Escherichia coli	PFAM: Rhodanese-like domain	hypothetical protein	human (fragment)	PFAM: Poly A polymerase family	CGI-47 PROTEIN.		PFAM: Kelch motif	(T.	JNG JNG	PROTEIN.		PFAM: Kelch motif	LYMPHOCYTE	ACTIVATION-	ASSOCIATED PROTEIN.	PFAM:
	HMMER	2.1.1	blastx.2	HMMER 2.1.1	blastx.2		HMMER 2.1.1	blastx.2		HMMER 2.1.1	blastx.2		HMMER 2.1.1	blastx.2				HMMER 2.1.1	blastx.2			HIMMER
	510			511		•	512	-		513			514					515				516
	955895			956046	··		959377			960354			960951			1		960955				961002
_	HDTEN41			HSDDD20			HDPBL08			HMELJ75			HLTCU08				2	HIOHK41				HTKAA03
											_											

1	-		2.1.1	Fumarylacetoacetate				
				(FAA) hydrolase family				
			blastx.2	probable 2-hydroxyhepta-	pir A64864 A64864	%86	2	202
			_	2,4-diene-1,7-dioate				
				isomerase b1180 -				
				Escherichia coli				-
9	962420	517	HMMER	PFAM: Glycosyl	PF01532	38.1	198	323
		٠.	2.1.1	hydrolase family 47				
			blastx.2	CDNA FLJ10783 FIS,	sp BAA91806 BAA9	%06	204	332
				CLONE NT2RP4000417,	1806	34%	16	204
		-		WEAKLY SIMILAR TO				
				1				
9	963511	518	HMMER 2.1.1	PFAM: Kelch motif	PF01344	151.1	69	212
			blastx.2	ACTIN-BINDING	sp Q9Y573 Q9Y573	100%	3	443
				PROTEIN.	, -	32%	9	440
						300%	7	401
						300%	0	277
						2070	40	//0
				,		30%	228	440
						100%	446	490
						54%	452	484
9	964035	519	HIMMER 2.1.1	PFAM: AhpC/TSA family	PF00578	247.1	108	575
			blastx.2	ANTIOXIDANT	sp P30041 AOP2 HU	100%	. 93	761
				PROTEIN 2 (EC 1.11.1.7)	MAN			
				(24 KDA PROTEIN) 1				
6	965585	520	HIMMER	PFAM:	PF01557	100.2	495	292
			2.1.1	Fumarylacetoacetate				
				(FAA) hydrolase family				
_			blastx.2	CGI-105 PROTEIN.	sp Q9Y3B0 Q9Y3B0	%16	546	214

			T	т—	Т		1			Т			Τ	T			
375	438	207	411	341	1193	1216	282	321	279	279	347	448	429	138	258	255	497
160	154	151	199	174	3	1178	52	1	193	1	246	407	286	4	4		111
33.4	55%	8.34	60%	63.4	%66	%69	27.2	71%	26.4	38%	41%	21%	42.7	30.2	46%	43%	102.6
PF00534	904V90 Q9VP06	PF00010	sp Q9Y5A8 Q9Y5A8	PF01846	gb AAD42862.1 AF1	55096_1	PF00583	sp CAA04463 CAA0 4463	PF00899	sp BAA94076 BAA9	4076		PF01344	PF00850	pir T46284 T46284		PF00583
PFAM: Glycosyl transferases group 1	CG11306 PROTEIN.	PFAM: Helix-loop-helix DNA-binding domain	NY-REN-6 ANTIGEN (FRAGMENT).	PFAM: FF domain	(AF155096) NY-REN-6	antigen [Homo sapiens]	PFAM: Acetyltransferase (GNAT) family	EMeg32 protein.	PFAM: ThiF family	Ubiquitin-activating	enzyme E1.		PFAM: Kelch motif	PFAM: Histone deacetylase family	hypothetical protein	DKFZp566E044.1 - human	PFAM: Acetyltransferase (GNAT) family
HMMER 2.1.1	blastx.2	HMMER 1.8	blastx.2	HMMER 2.1.1	blastx.2		HMMER 2.1.1	blastx.2	HIMMER 2.1.1	blastx.2			EIMMER 2.1.1	HMMER 2.1.1	blastx.2		HMMER 2.1.1
521		522		878			523		524				525	526			527
965611		954723		966294			696996		967483				967593	971428			974402
HE2SB11		HCFLJ17		HCFLJ17			HLICJ19		HDPSM18				HMAKJ82	HFPIX37	,		HHEKP47
								514									

			blastx.2	phnO protein - Escherichia coli	pir G35719 G35719	100%	96	527
HTPDV62	418671	528	HMMER 2.1.1	PFAM: Guanylate kinase	PF00625	41.6	2	109
			blastx.2	guanylate kinase (EC 2.7.4.8) 1 - human	pir S68864 S68864	100%	200	109
HUSAJ73	567234	529	HIMMER 2.1.1	PFAM: POLO box duplicated region.	PF00659	26.4	31	126
			blastx.2	SERUM-INDUCIBLE KINASE	6L9090 6L9090 ds	%16	31	159
						57%	413	589
HSKCJ76	747380	530	HMMER 2.1.1	PFAM: POLO box duplicated region.	PF00659	86	115	306
			blastx.2	SERUM-INDUCIBLE KINASE.	619090 619090 ds	95%	115	321
нсвох38	881200	531	HMMER 2.1.1	PFAM: CNH domain	PF00780	68.9	105	386
			blastx.2	Misshapen/NIK-related kinase MINK-1.	sp BAA90753 BAA9 0753	95%	120	386
HFICR59	911317	532	HMMER 2.1.1	PFAM: Guanylate kinase	PF00625	141.3	221	493
			blastx.2	MAGUK protein VAM-1.	sp AAD45919 AAD4 5919	100%	2	721
HPDV067	911405	533	HMMER 2.1.1	PFAM: Guanylate kinase	PF00625	46.4	211	396
	w		blastx.2	20-3.	sp 095049 095049	%88	-	726
						26%	629	784
				-		%89	069	755
	0,001,01	1				20%	387	446
nzLAD33 .	952181	534	HMMER	PFAM: Guanylate kinase	PF00625	8.69	7	177

	360	711	771	761	1097					-				378	270	0/0		700	¥07	416
		16		423	33			147		177				211	300	7007		C.	70	207
	100%	183.7	94%	62.3	94%			54.3	•	100%				53.4	7008			07.2		100%
	sp AAF63789 AAF63	PF00780	sp Q9Y6R5 Q9Y6R5	PF01712	gi 4191348 gb AAD0	9755.1		PF01118	•	pir/A00364 DEECDA				PF01118	DINA00364[DFFCDA			DE01689		pir F64762 F64762
	PALS1.	PFAM: CNH domain	GERMINAL CENTER KINASE RELATED PROTEIN KINASE.	PFAM: Deoxynucleoside kinase	(AF087661) NADH-	ubiquinone	subunit [Homo sapiens]	PFAM: Semialdehyde	dehydrogenase	aspartate-semialdehyde	dehydrogenase (EC	1.2.1.11) - Escherichia	coli	PFAM: Semialdehyde	aspartate-semialdehvde	dehydrogenase (EC	1.2.1.11) - Escherichia	PFAM:	Hydratase/decarboxylase	probable hydratase (EC 4.2.1) mhpD -
2.1.1	blastx.2	HMMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.14			HMMER	2.1.1	blastx.2				HIMMER 2.1.1	blastx.2			HIMMER		blastx.2
		535	····	882				537						538				539		
		954181	;	971074				499457						513261				527840		
		HETLM90	·	HCESE94				HFXCU55						HEPBV24				HFRAU96		·

549	52	377		458		416		464	33			231		741	100	684	0.0	858					350			374		
418	2	78		78		36		33		ı		88		82	1,00	82/	150	751	_		-		6			6		
%95	.%0∠	49		77%		218.9		79%	100%			24.5		85%	700	9.07	1000/	100%					186.1			100%		_
		PF00668		pir H64/91 YGECEF		PF01619	,,	sp[043272 PROD H	UMAN			PF00953	-	pir C65182 C65182	DE00052	FF00933	11 08 C76 780 11	gu AAC/0/03.1					PF01571			sp Q9UI17 Q9UI17	,	
Escherichia coli		PFAM: Domain of	מומוסושיו ומוסווסוו	enterobacin synthetase component F -	Escherichia coli	PFAM: Proline	dehydrogenase	PROLINE OXIDASE,	MITOCHONDRIAL	PRECURSOR (EC 1.5.3) 1	PFAM: Glycosyl	transferase	probable undecaprenyl-	DFAM: Glacomil	Transferase	(AF000454) ITDP.	(ACCOUNT)	GlcNAc:undecaprenylpho	sphate GlcNAc-1-	phosphate 1 [Escherichia	coli]	PFAM: Glycine cleavage	1-protein (aminomethyl	transferase)	DIMETHYLGLYCINE	DEHYDROGENASE	PRECURSOR (EC
		HMMER	110011	Diastx.2		HMMER	2.1.1	blastx.2				HMMER	2.1.1	blastx.2	HAMAFE	2.1.1	hlasty 2	Diam'r.					HMMER	7.1.7		blastx.2		
		540				541						542			883	5							543		***			
		527944				536558						828609		· · · · · · · · · · · · · · · · · · ·	961693	20107							661483					
	o o de de de de de de de de de de de de de	HTLBD23				HCEBM51						HSLFF79			HSI FF79					-			HKTAB71					

				15992).				
HSDIF25	678003	544	HMMER	PFAM: Tetrahydrofolate	PF00763	282.6	51	425
			1:1:7	olase				
			blastx.2	methylenetetrahydrofolate	pir H64784 JS0662	%86	45	425
				dehydrogenase (NADP+)		82%	409	495
				(EC 1.5.1.5) 1 -				
HNTHTW/82	684347	545	HWMER	PFAM: Dehydratase	PF00920	34.2	183	266
70 11	71.00	<u>.</u>	2.1.1	family				
			blastx.2	probable dihydroxy-acid	pir/E64752/E64752	%06	1	195
				dehydratase yagF -	-	100%	183	284
				Escherichia coli		70%	93	122
HFATN41	712097	546	HIMMER	PFAM: Dihydroorotate	PF01180	203.7	304	069
			2.1.1	dehydrogenase				
			blastx.2	dihydroorotate oxidase	pir/A23109 DEECDO	%28	298	729
_				(EC 1.3.3.1) - Escherichia		%56		596
				coli				
HHFFG80	733387	547	HMMER	PFAM:	PF01762	28.3	179	427
			2.1.1	Galactosyltransferase				
			blastx.2	T7N9.18.	sp AAF79857 AAF79	30%	∞	478
					857			
HSDFF73	761657	548	HMMER	PFAM: Prephenate	PF00800	75.3	3	200
			2.1.1	dehydratase				
			blastx.2	chorismate mutase (EC	pir/A30261/KMECP	82%	3	488
					W			
				dehydratase (EC 4.2.1.51)				
				pheA [validated] -				
			-	Escherichia coli				
HTI.BH79	774422	549	HMMER	PFAM:	PF01762	115.2	252	545
· · · · · · · · · · · · · · · · · · ·		-						

HTLBH79 797621 884 HAMGER PRAM: PRO1702YLTRANNSF PRO1702 98.5 616 356 HTLBH79 797621 884 HAMGER PRAM: PRO1702 98.5 616 356 HTLBH79 971837 885 HAMGER PRAM: Galactosyltransferase PRO1702 112.9 349 663 HBWCD80 777346 550 HAMGER PRAM: Lysyl hydrolase PRO2002 45 341 568 HSDK189 786812 551 HAMGER PRAM: Lysyl hydrolase PRO1315 1952 3 443 HBDA29 810879 552 HAMGER PRAM: Dihydrocrotase PRO0744 590 400% 804 206 HBMCD80 777346 551 HAMGER PRAM: Lysyl hydrolase PRO1315 1952 3 443 HBDA29 810879 552 HAMGER PRAM: Dihydrocrotase PRO0744 30.1 170 331 HBDA29 810879 552 HAMGER PRAM: Dihydrocrotase PRO1744 85% 25 460 HLDQU68 825558 553 HAMGER PRAM: Dihydrocrotase PRO1619 92.2 46 408 HLDQU68 825558 553 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 like PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 dahydrogenase PRO1619 92.2 46 408 2.1.1 dahydrogenase PRO1619 PRO1619 92.2 46 408 2.1.1 dahydrogenase PRO1619 PRO1619 92.2 46 408 2.1.1 dahydrogenase PRO1619 PRO1619 92.2 46 408 2.1.1 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 HAMGER PRAM: Dihydrogenase PRO1619 92.2 46 408 2.1.1 HA				2.1.1	Galactosyltransferase				
BRASE 1 1 1 PF01762 98.5 616				blastx.2	GANGLIOSIDE	sp O96024 O96024	%86	12	545
9 971837 884 HMMER PEAM: PF01762 98.5 616 9 971837 885 HMMER PFAM: Calactosyltransferase PF01762 112.9 349 9 971837 885 HMMER PFAM: CAB026730) beta 1,3- dbjjBAA88988.1 97% 340 1 HAMER PFAM: Lysyl hydrolase PF02062 45 341 1 HAMER PFAM: Lysyl hydrolase PF02062 45 341 1 PRAM: Lysyl hydrolase PF02062 45 341 2 L.1. Libration W5 W5 864 ADHESION W5 W5 40% 864 ADHESION W5 ADHESION W5 146 ABSB12 551 HMMER FFAM: Aldehyde oxidase PF01315 195.2 3 CERT: CHENAL: CHENAL: ADHESION W5 195.2 3 Blastx. Probabile oxidoreductase PF00744 85% 20 110 <tr< td=""><td></td><td></td><td></td><td></td><td>GALACTOSYLTRANSF</td><td></td><td></td><td></td><td></td></tr<>					GALACTOSYLTRANSF				
1717346 1717	UTT DU70	707621	100	HYWEB	DEAM:	DE01762	98 5	616	356
971837 885 HMMER PFAM: PFOIT 62 112.9 349 2.1.1 Galactosyltransferase dbjBAA88988.1 97% 340 2.1.1 Galactosyltransferase-4 dbjBAA88988.1 97% 340 340 galactosyltransferase-4 FROZO62 45 341 400 550 HMMER PFAM: Lysyl hydrolase PF02062 48 341 ADHESION W5 ADHESION W5 40% 864 ADHESION W5 ADHESION 40% 864 MOLECULE. ADHESION W5 195.2 3 ABABIA PRAM: Aldehyde oxidase PF01315 195.2 3 CECL:) yagR (ECL) yagR (ECL) yagR (ECL) yagR 552 HMMER PFAM: Dilydroorotase- PF00744 80% 26 Blastx.2 Collapsin response SplAAF80348 AAF80 80% 26 Blastx.2 Collapsin response SplO1619 92.2 46 Blastx.2 Gehydrogenase <td>(11197111</td> <td>12/021</td> <td>†</td> <td>2.1.1</td> <td>Galactosyltransferase</td> <td></td> <td>)</td> <td>9</td> <td>)</td>	(11197111	12/021	†	2.1.1	Galactosyltransferase)	9)
2.1.1 Galactosyltransferase dbjBAA88988.1 97% 340 blastx.2 (AB026730) beta 1,3- dbjBAA88988.1 97% 340 galactosyltransferase-4 [Homo sapiens] 45 341 [Homo sapiens] PFAM: Lysyl hydrolase PF02062 45 341 2.1.1 CEREBRAL CELL sp Q9UMW5 Q9UM 48% 146 ADHESION W5 40% 864 MOLECULE. W5 40% 864 ADHESION W5 195.2 3 ADHESION W5 195.2 3 ADHESION W5 195.2 3 ADHESION W5 195.2 3 ADHESION W5 195.2 3 ADHESION W5 195.2 3 ADHESION W5 195.2 3 ADHESION W5 195.2 3 Blastx.2 plastx.2 probable oxidoreductase pripO4754pbAF80348pAF80 80% 26 Blastx.2 </td <td>HTLBH79</td> <td>971837</td> <td>885</td> <td>HMMER</td> <td>PFAM:</td> <td>PF01762</td> <td>112.9</td> <td>349</td> <td>663</td>	HTLBH79	971837	885	HMMER	PFAM:	PF01762	112.9	349	663
Piastx.2 AB026730 beta 1,3- Abj BAA88988.1 97% 340				2.1.1	Galactosyltransferase				
Elemon sapiens Elemon sap				blastx.2	(AB026730) beta 1,3-	dbjBAA88988.1	%16	340	798
Homo sapiens Homo sapiens					galactosyltransferase-4				
777346 550 HMMER PFAM: Lysyl hydrolase PF02062 45 341					[Homo sapiens]				
Note	HBWCD80	777346	550	HIMMER 2.1.1	PFAM: Lysyl hydrolase	PF02062	45	341	268
ADHESION Wish A0% 864				blastx.2	CEREBRAL CELL	MU6913WMU691qs	48%	146	937
786812 551 HMMER PFAM: Aldehyde oxidase PF01315 195.2 3 2.1.1 and xanthine dehydrogenase, C terminus 85% 3 blastx.2 probable oxidoreductase pir D64754 D64754 85% 3 (EC 1) yagR [similarity] - Escherichia 30.1 170 810879 552 HMMER PFAM: Dihydroorotase- PF00744 30.1 170 blastx.2 Collapsin response sp AAF80348 AAF80 80% 26 blastx.2 Collapsin response sp AAF80348 AAF80 80% 26 mediator protein-5 348 53% 418 2.1.1 dehydrogenase PF01619 92.2 46					ADHESION	W5	40%	864	926
786812 551 HMMER PFAM: Aldehyde oxidase PF01315 195.2 3 2.1.1 and xanthine dehydrogenase, C 85% 3 terminus terminus 85% 3 blastx.2 probable oxidoreductase pir D64754 D64754 85% 3 (EC 1) yagR (EC 1) yagR 20li 170 similarity] - Escherichia coli 170 blastx.2 Collapsin response PF00744 30.1 170 blastx.2 Collapsin response sp AAF80348 AAF80 80% 26 blastx.2 Collapsin response sp AAF80348 AAF80 80% 26 thike plastx.2 PAM: Proline PF01619 92.2 46 state 2.1.1 dehydrogenase PF01619 92.2 46					MOLECULE.			_	
2.1.1 and xanthine dehydrogenase, C terminus blastx.2 probable oxidoreductase (EC 1) yagR [similarity] - Escherichia coli 2.1.1 like blastx.2 Collapsin response blastx.2 Collapsin response blastx.2 Collapsin response blastx.2 RMMER PFAM: Proline sepsential dehydrogenase brought of the properties of the prolific of the prolific of the proline sepsential dehydrogenase collapsin response blastx.2 Collapsin response sp AAF80348 AAF80 80% 26 sp AAF80348 AAF80 80% 26 sp AAF80348 AAF80 80% 26 sp AAFB0348 AAF80 80% 26 sp AAFB0348 AAF80 80% 26 sp AAFB0348 AAF80 80% 26 sp AAFB0348 AAF80 80% 26 sp AAFB0348 AAF80 80% 26 sp AAFB0348 AAF80 80% 26 sp AAFB0348 AAF80 80% 26 sp AAFB0348 AAF80 80% 26 sp AAFB0348 AAF80 80% 26 sp AAFB0348 AAF80 80% 26 sp AAFB0348 AAF80 80% 26 sp AAFB0348 AAFB0 80% 26 sp AAFB0348 AAFB0 80% 26 sp AAFB0348 AAFB0 80% 26 sp AAFB0348 AAFB0 80% 26 sp AAFB0348 AAFB0 80% 26 sp AAFB0348 AAFB0 80% 26 sp AAFB0348 AAFB0 80% 26 sp AAFB0348 AAFB0 80% 26 sp AAFB0348 AAFB0 80% 26 sp AAFB0348 AAFB0 80% 26 sp AAFB0348 AAFB0 80% 26 sp AAFB	HSDKI89	786812	551	HMMER	PFAM: Aldehyde oxidase	PF01315	195.2	n	443
dehydrogenase, C				2.1.1	and xanthine			•	
Hastx.2 Probable oxidoreductase Pir D64754 D64754 85% 3					dehydrogenase, C			-	
Plastx.2 Probable oxidoreductase Pir D64754 D64754 85% 3					terminus				
Rec 1) yagR Escherichia Coli Coli Coli Iike Dihydroorotase- PF00744 So.1 170 So.1.1 Iike Diastx.2 Collapsin response Sp AAF80348 AAF80 So.26 So.2558 So.3 HMMER PFAM: Proline PF01619 PF01619 PF01619 So.2 Aforagenase PF01619 PF01				blastx.2	probable oxidoreductase	pir D64754 D64754	85%	n	200
Since Escherichia Escherichia Coli Coli Escherichia Coli Escherichia Escherichia Since Coli Escherichia Since Sinc					(EC 1) yagR				
810879 552 HIMMER PFAM: Dihydroorotase- PF00744 30.1 170 2.1.1 like sp AAF80348 AAF80 80% 26 blastx.2 Collapsin response sp AAF80348 AAF80 80% 26 mediator protein-5. 348 53% 418 HIMMER PFAM: Proline PF01619 92.2 46 2.1.1 dehydrogenase 46 46					[similarity] - Escherichia				
2.1.1 like blastx.2 Collapsin response sp AAF80348 AAF80 80% 26 mediator protein-5. 348 53% 418 825558 553 HMMER PFAM: Proline PF01619 92.2 46 21.1. dehydrogenase	HIBDA29	810879	552	HIMMER	PFAM: Dihydroorotase-	PF00744	30.1	170	331
blastx.2 Collapsin response sp AAF80348 AAF80 80% 26 mediator protein-5. 348 53% 418 825558 553 HMMER PFAM: Proline PF01619 92.2 46 2.1.1 dehydrogenase 46				2.1.1	like				
825558 553 HMMER PFAM: Proline PF01619 92.2 46 2.1.1 dehydrogenase 46				blastx.2	Collapsin response	sp AAF80348 AAF80	%08	26	460
825558 553 HMMER PFAM: Proline PF01619 92.2 46 2.1.1 dehydrogenase					mediator protein-5.	348	53%	418	507
	HLDQU68	825558	553	HIMMER	PFAM: Proline	PF01619	92.2	46	408
				2.1.1	dehydrogenase				

453	340	382	294	405	681	681	185		268	703	724	685	700
	32	44	199	22	274	187	8		155	86	77	362	269
91%	206.4	%99	27.7	37%	200.1	79%	100%		29.2	31%	28%	119.7	97%
sp Q9UF12 Q9UF12	PF01210	sp O57656 GPDA_F UGRU	PF01301	sp Q9VGE7 Q9VGE7	PF00549	pir A90499 SYECSA			PF01011	pir H69064 H69064		PF01243	sp BAA91668 BAA9 1668
KIDNEY AND LIVER PROLINE OXIDASE 1.	PFAM: NAD-dependent glycerol-3-phosphate dehydrogenase	GLYCEROL-3- PHOSPHATE DEHYDROGENASE [NAD+], CYTOPLASMIC 1	PFAM: Glycosyl hydrolases family 35	CG3132 PROTEIN.	PFAM: CoA-ligases	succinateCoA ligase	(ADP-forming) (EC	6.2.1.5) alpha chain - Escherichia coli	PFAM: PQQ enzyme repeat	serine/threonine protein	kinase related protein - 1	PFAM: Pyridoxamine 5'-	CDNA FLJ10535 FIS, CLONE NT2RP2001070, WEAKLY SIMILAR TO
blastx.2	HMMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.2	HMMER 2.1.1	blastx.2			HMMER 2.1.1	blastx.2		HMMER 2.1.1	blastx.2
	554		555		556				557			558	
	827510		837509		847314				850577			852701	
	HMUAS41		нтхон20		HSLFG13				HDAAS21			HARMH10	

	decarboxylase ornithine decarboxylase ninA4083
οάΥ.	ornithine decarboxylase (EC 4.1.1.17), inducible
	Escherichia coli
.0go	PFAM: Carbon-nıtrogen hydrolase
V	BETA-
4 8	DEAM. Corbon pitrogen
Ž0	JOIL-III
]	
AS	UREIDOPROPIONASE
_	PFAM: Glycosyl hydrolases family 31
حل	hypothetical 77.2 kD
نت	protein in glnA-fdhE
	intergenic region -
äir	Escherichia coli (strain K- 12)
138	PFAM: Biotin synthase
ان	biotin synthetase (EC
a	2.8.1) - Escherichia coli
	PFAM: Bacterial
잂	Cytochrome Ubiquinol
Ĭį.	cytochrome d ubiquinol
7	Oxidage (FC 1 10 2 _)

				chain I - Escherichia coli		100%	339	419
						81%	419	451
HMAEM27	870252	565	HMMER 2.1.1	PFAM: tRNA synthetases class I (R)	PF00750	24.6	531	716
-			blastx.2	CG8097 PROTEIN.	0TXV6Q0VXT0	31%	291	716
HEBCK42	875541	995	HMMER	PFAM: Inorganic	PF00719	2.69	317	445
			blastx.2	inorganic	pir A45153 A45153	100%	317	445
				pyrophosphatase (EC 3.6.1.1) - bovine				
HELFN03	881180	567	HMMER 2.1.1	PFAM: Carbon-nitrogen hydrolase	PF00795	64.3	461	733
			blastx.2	ybeM protein - Escherichia coli	pir H64796 H64796	93%	383	733
HKIMF95	882308	568	HMMER	PFAM: Delta 1-pyrroline-	PF01089	41.1	46	222
			blastx.2	hypothetical protein M153.1 - Caenorhabditis	pir T23765 T23765	46%	49	222
70000	670000	023	THATED	elegans DDAM: Ditxidrocrotese	DE00744	1327	-	549
HILHE83	683203	506	2.1.1	like	110011		•	,
			blastx.2	Hypothetical 61.4 kDa	sp CAB95124 CAB9	%16	1	582
				protein.	5124	72%	515	721
HTEOE72	886412	570	HMMER	PFAM: Fucosyl	PF00852	83.4	115	498
			blastx.2	CG4435 PROTEIN.	sp Q9VLC1 Q9VLC1	47%	100	009
HELBN13	907599	571	HMMER	PFAM: Aconitase C-	PF00694	178.3	330	626
			2.1.1	terminal domain				
			blastx.2	ACONITATE	sp P25516 AC01_EC	100%	330	644

354	112	715	1352	1212	1313	1565	307	160	700	06/	000	68/	5	301		904		904	263	;	369	•		,	516		
106	2	629	1708	1450	1450	1705	161	101	-		3,6	362	200	477		230		242	96		235				211		
%68	94%	100%	46.4	700	47%	36%	37	/0	1010	01% 		48	1000	53%	İ	397.5		100%	25%		25.3				%98		
OLI			PF00849		sp O66114 YLP4_ZY	MMO	PEO1 411	PF01411		sp Q9W4R9 Q9W4K o		PF00753		pir ₍ JC5826/JC5826		PF01268		pir T17244 T17244			PF01135				sp BAA91877 BAA9 1877		
HYDRATASE 1 (EC	4.2.1.3) (CITRATE	HYDRO-LYASE 1	PFAM: RNA	pseudouridylate synthase	HYPOTHETICAL 24.4	LPD	3 REGION (ONT4).	NA synthetases		CG10802 PROTEIN.		PFAM: Metallo-beta-	Jactainase superrainery	hydroxyacylglutathione hydrolase (EC 3.1.2.6) -	rat	PFAM: Formate-	tetrahydrofolate ligase	hypothetical protein	DKFZp586G1517.1 -	human (fragment)	PFAM: Protein-L-	isoaspartate(D-aspartate)	O-methyltransferase	(PCMT)	CDNA FLJ10883 FIS, CLONE NT2RP4001946,	WEAKLY SIMILAR TO	1
			HIMMER	2.1.1	blastx.2			HMMER	2.1.1	blastx.2		HIMIMER 7 1 1	2.1.1	blastx.2		HMMER	2.1.1	blastx.2			HMMER	2.1.1			blastx.2		
			572					573			İ	574				575					576						
			914882					915743				917409				917564					920288					,	
			HFIJE03					HABGE01				HWLKM02				HOVER13	STORE OF THE				HE8UB94						

1505	1691		289	702					288		264	412		1760		1760		137			224		295		280
1404	1401		499	472					40		19	329		291		594		45			3		750		819
32.4	39%		55.6	45%				-	30.8		93%	%09		374.8		%96		45.2			%86		242.6		78%
PF01011	sp BAA97455 BAA9	7455	PF00750	pir T39985 T39985					PF00750		sp CAB76858 CAB7	8589		PF00750		sp CAB76858 CAB7	6858	PF00678			sp CAB89810 CAB8	9810	PF00549		sp Q9UNP6 Q9UNP6
PFAM: PQQ enzyme repeat	Genomic DNA,	chromosome 5, BAC clone:F14A1.	PFAM: tRNA synthetases class I (R)	probable arginyl-trna	synthetase, cytoplasmic -	fission yeast	(Schizosaccharomyces	pombe)	PFAM: tRNA synthetases	class I (K)	DJ382I10.5.1 (novel	protein similar to arginyl-	tRNA 11	PFAM: tRNA synthetases	class I (R)	DJ382I10.5.1 (novel	protein similar to arginyl-	PFAM: Short chain	dehydrogenase/reductase	C-terminus	Alcohol dehydrogenase,	short chain.	PFAM: CoA-ligases		SUCCINYL-COA
HMMER 2.1.1	blastx.2		HMMER 2.1.1	blastx.2					HMMER	[2.1.1]	blastx.2			HMMER	2.1.1	blastx.2		HMMER	2.1.1		blastx.2		HMMER	2.1.1	blastx.2
577	_		578		1.				579					580				581					582		
921274			922580						922581					922582				924110					926401		
HTHDJ23			HWHPB72						HSQFX64	-				HDABB84				HLHFN83					HPCRR26		

To
SYNTHETASE ALPHA 153 692 599
SYN SUB Blastx.2 B7A Blastx.2 B3 Blastx.2 B1 B1AMER PFA B1AMER PFA B1AMER PFA B1AMER PFA B1AMER PFA B1AMER PFA B1AMER PFA B1AMER B1 B1AMER B1AMER B1AMER B1AMER B1AMER B1AM
HEGDE HEGDE HEGDE HEGDE HEGALE HE HEGALE HE HEGALE HE HEGALE HEGALE HE HEGALE HE HE HE HE HE HE HE HE HE HE

_				blastx.2	CG3132 PROTEIN.	sp O9VGE7 Q9VGE7	%65	2	196
							40%	311	496
L	HNGKH38	951032	589	HMMER	PFAM: Delta 1-pyrroline-	PF01089	46.8	3	209
				2.1.1	5-carboxylate reductase				
				blastx.2	CG5840 PROTEIN.	sp Q9VEJ3 Q9VEJ3	43%	12	212
L	HNHNN26	952398	290	HMMER	PFAM: Magnesium	PF01078	91.1	191	406
				2.1.1	chelatase, subunit Chil				
				blastx.2	hypothetical 56.2K	pir/JQ0872/JQ0872	85%	191	406
					protein (ilvG-rmC		18%	33	158
					intergenic region) - Escherichia coli		72%	8	40
L	HTEHP64	953791	591	HMMER 2.1.1	PFAM: Asparaginase	PF01112	32.1	198	404
				blastx.2	asparaginase (EC 3.5.1.1)	pir S22523 S22523	40%	3	281
					[validated] - tree lupine		48%	294	497
 26					(fragment)		28%	101	202
	-						36%	333	407
l	HMIAO78	953793	592	HMMER 2.1.1	PFAM: Asparaginasè	PF01112	71.3	316	486
				blastx.2	Putative 1-asparaginase.	sp CAC09349 CAC0	%95	316	486
						9349	40%	162	326
							32%	482	577
l	HFPCN94	600556	593	HMMER	PFAM: CDP-alcohol	PF01066	94.1	366	830
			·	blastx.2	DJ967N21.6 (NOVEL	spl09UJA2 09UJA2	77%	84	860
					CDP-ALCOHOL	,			
					PHOSPHATIDYLTRAN				
					SFERASE FAMILY 1				
<u> </u>	HSLHV08	958582	594	HMMER	PFAM: Gamma-	PF01019	30.8	11	166
_		-		2.1.1	glutamyltranspeptidase				

			blastx.2	gamma-	nir/IV0028/FKFCFY	7077	-	1
				glutamyltransferase (EC		8/00	1)	100
				2.3.2.2) precursor - Escherichia coli				
HPDVW40	961039	595	HMMER	PFAM: Adenylosuccinate	PF00709	458.6	9	533
			2.1.1	synthetase				
			blastx.2	ADENYLOSUCCINATE SYNTHETASE,	splP28650 PUA1_M OUSE	%88	3	629
				MUSCLE ISOZYME (EC 6.3.4.4) 1				~
HEMFC70	961963	.965	HMMER 2.1.1	PFAM: Ubiquitin carboxyl-terminal	PF01088	32.5	664	798
				hydrolase, family 1				
			blastx.2	AD-019 protein.	sp AAF67486 AAF67 486	%66	217	1164
	910371	297	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	9.29	132	52
HLD0020	963284	988	HMMER 2.1.1	PFAM: Urocanase	PF01175	175.9	12	1205
			blastx.14	urocanate hydratase	gi 21965 emb CAA48	32%	747	1196
				[Trifolium repens]	765.1	31%	12	569
						38%	543	692
						%09	282	326
+	0,000	t				24%	327	485
07000711	963635	287	HMMER 2.1.1	PFAM: Urocanase	PF01175	165	-	1188
			blastx.14	e e	gi 21965 emb CAA48	32%	730	1179
				[Infolum repens]	765.1	38%	526	675
			_	•		78%		252
-						%09	265	309

HSLEP67	963505	865	HMMER 2.1.1	PFAM: ThiJ/PfpI family	PF01965	52.9	107	238
		_	blastx.2	hydroxymethylpyrimidine	pir H64771 H64771	%86	113	352
				kinase (EC 2.7.1.49) - Escherichia coli		75%	92	123
HSLEP94	964463	599	HMMER 2.1.1	PFAM: Asparaginase	PF01112	543.1	444	1292
			blastx.2	probable asparaginase (EC	pir[D64820]D64820	%46	441	1292
				3.5.1.1) ybiK - Fscherichia coli		93%	1292	1336
HSENS89	964527	009	HMMER	PFAM: Formate	PF01268	637.3	43	876
			2.1.1	tetrahydrofolate ligase				
			blastx.2	hypothetical protein	pir T17244 T17244	75%	37	1050
				DKFZp586G1517.1 - human (fragment)		-		!
HNTAF77	966190	109	HIMMER	PFAM: Peptidyl-tRNA	PF01195	100.1	3	275
			2.1.1	hydrolase				
-			blastx.2	aminoacyl-tRNA	pir S75738 S75738	52%	3	215
				hydrolase (EC 3.1.1.29) -				
				Synechocystis sp. (strain				
			1	FCC 0803)	0101010	033	300	150
HBIOV48	967566	709	HMMER 2.1.1	PFAM: Gamma- glutamyltranspeptidase	Pr01019	55.5	C67	0004
			blastx.2	DJ18C9.2 (NOVEL	sp Q9UJ14 Q9UJ14	84%	148	450
				GENE (LOCUS		%92	65	154
				D20S101) SIMILAR TO		25%	9	107
				11		73%	468	530
HBGMN45	967744	603	HMMER	PFAM: Oxidoreductase	PF01408	129.4	7	454
			2.1.1	family				000
			blastx.2	ycjS protein - Escherichia	pir F64880 F64880	84%	2	688

				coli				
HBXCE20	688026	604	HMMER 2.1.1	PFAM: MoaC family	PF01967	178.9	116	370
			blastx.2	molybdenum cofactor biosynthesis protein C (validated) - Escherichia	pir G64814 G64814	%08	44	403
				coli			0,1	1
HSLJU88	780811	905	HMMER 2.1.1	PFAM: tRNA synthetases class I (E and Q)	PF00749	26.3	448	537
			blastx.2	dihydroorotate oxidase	pir/A23109 DEECDO	100%	449	3
		<u> </u>		(EC 1.3.3.1) - Escherichia coli				
HKGDQ60	863330	909	HMMER	PFAM: tRNA synthetases class I (E and O)	PF00749	193.4	114	458
			blastx.2	CG4573 PROTEIN.	8p Q9VV59 Q9VV59	63%	117	446
						41%	460	750
HSDKF67	933059	209	HMMER 2.1.1	PFAM: tRNA synthetases class I (E and O)	PF00749	274.1	7	451
			blastx.2	glutaminetRNA ligase	pir G64802 SYECQT	%86	2	451
				(EC 6.1.1.18) [validated] - Escherichia coli				
HSLFT94	603023	809	HMMER 2.1.1	PFAM: PAP2 superfamily	PF01569	72.8	15	302
			blastx.2	phosphatidylglycerophosp hatase (EC 3.1.3.27) B -	pir A30193 PAECGB	100%	m.	314
	000	1	day 6 ar	DEAM. Transfel	DE00783	246.8	20	424
HIJMD06	83/603	600	FIMILIER	FFAM: mositor	C0/00.11	0.01	3	1
			2.1.1	polypilospilate nhosphatase family.				
				catalytic domain				
_	_	_						

		-	blastx.2	SYNAPTOJANIN 2 (EC	sp O15056 SY12_HU MAN	97%	14	433
HNTBH68	851274	610	HMMER 2.1.1	PFAM: PAP2 superfamily	PF01569	50.6	16	420
			blastx.2	CDNA FLJ20300 FIS, CLONE HEP06465.	sp BAA91072 BAA9 1072	21%	1	540
HMEK039	863507	611	HMMER 2.1.1	PFAM: PAP2 superfamily	PF01569	26.2	269	550
	· · · · · · · · · · · · · · · · · · ·		blastx.2	CDNA FLJ20300 FIS, CLONE HEP06465.	sp BAA91072 BAA9 1072	49%	2	619
HAABH11	965473	612	HMMER 2.1.1	PFAM: PAP2 superfamily	PF01569	38.2	298	663
			blastx.2	CG12746 PROTEIN.	sp Q9VNDS Q9VND 5	46%	46	999
HUVFZ43	910860	613	HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	164.4	9	401
			blastx.2	MAP kinase phosphatase.	sp BAA89534 BAA8 9534	%95	3	494
HCEPH84	910864	614	HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	136.4	1158	727
			blastx.2	PROTEIN PHOSPHATASE.	э <u>л</u> гоб)ј <u>лго</u> б)јаз	%05	1251	757
HNFDO52	916260	615	HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	92.1	2	358
			blastx.2	dual specificity phosphoprotein phosphatase (EC 3.1.3) 2	pir A57126 A57126	95%	257	130 358

	_			- himan				
HHEJR23	919082	616	HMMER 2.1.1	PFAM: Dual specificity phosphatase, catalytic domain	PF00782	52.2	426	253
			blastx.2	CG10371 PROTEIN.	sp Q9VCI6 Q9VCI6	42%	774	259
HMTAX31	971343	617	HMMER	PFAM: Dual specificity	PF00782	176.8	1064	651
		<u> </u>	2.1.1	phosphatase, catalytic domain				
			blastx.2	Mitogen-activated protein kinase phosphatase x.	sp AAF86649 AAF86 649	100%	1073	522
HKIYI74	729217	618	HMMER 2.1.1	PFAM: metallopeptidase family M24	PF00557	67.5	9	251
			blastx.2	CG5188 PROTEIN.	sp Q9VKV9 Q9VKV 9	51%	9 253	251 291
HSKEI21	760792	619	HMMER	PFAM: Aminopeptidase I	PF02127	118.8	201	398
			2.1.1	zinc metalloprotease				
				(M18)				
			blastx.2	ASPARTYL AMINOPEPTIDASE.	sp Q9ULA0 Q9ULA0	%06	138	473
HKAFK68	869127	620	HMMER 2.1.1	PFAM: Aminopeptidase I zinc metalloprotease	PF02127	190.4	216	506
			blastx.2	CDNA FLJ10915 FIS,	spBAA91903]BAA9	%86	117	909
				CLONE	1903	92%	529	570
				OVARC1000288,		46%	909	589
				WEAKLY SIMILAR TO				
HSRBB92	905110	621	HMMER 2.1.1	PFAM: UBX domain	PF00789	119.9	1757	2005
	17.20.50		blastx.2	CGI-03 PROTEIN (FAS-	sp Q9Y2Z3 Q9Y2Z3	93%	62	2011

	1 522	10 543	154 468	_	1 150			246 701		60 1595			100 315		1 342			13 207	_	246 440		609 1295	41 601	1050
						•																		1604
	245.2	%69	150	%96	%99			234.3		93%			88.8		84%			33.6		65.3		100%	91%	603
	PF00883	sp Q9V3D8 Q9V3D8	PF00557	sp P53582 AMP1 H	UMAN			PF00675		sp Q10713 MPPA_H	NTCTATO		PF00557		pir H65189 H65189			PF00636		PF00632		pir G64855 G64855		DE00270
ASSOCIATED FACTOR, FAF1).	PFAM: Cytosol aminopeptidase family	CG7340 PROTEIN.	PFAM: metallopeptidase family M74	PUTATIVE	METHIONINE	AMINOPEPTIDASE 1	(EC 3.4.11.18) 1	PFAM: Insulinase	(Peptidase family M16)	MITOCHONDRIAL	PEPTIDASE ALPHA	SUBUNIT 1	PFAM: metallopeptidase	family M24	X-Pro dipeptidase (EC	3.4.13.9) - Escherichia	coli (strain K-12)	PFAM: RNase3 domain.		PFAM: HECT-domain	(ubiquitin-transferase).	transcription/repair-	coupling protein - Escherichia coli	DEAM: DEAD/DEAU
	HMMER 2.1.1	blastx.2	HMMER	blastx.2				HIMIMER	2.1.1	blastx.2			HMMER	2.1.1	blastx.2			HMMER	7.1.1	HIMIMER	2.1.1	blastx.2		HAMAED
;	622		623		-			624					625			<u></u>		888		688		628		802
	931564		932577					942872					968439					883683		959570		266766		847655
	HWLLR80		HWLWQ87	 ,	_			H6EEP53	_				HE2KZ56					HFXHD52	,	HPMAM67		HBXFI75		HRYF175

ins ig P-loop) FACTOR ig P-loop) FACTOR Sp P49411 EFTU_HU 89% NDRIAL AAN 943. PF00270 In - human in PC0010 PC010 22% In - human in PC0010 PC010 In PC0270 In - human in PC0270 In - human in PC0270 In - human in PC0270 In - human in PC010 PC010 In PC027				2.1.1	box helicase				
1.8	HELGM94	913938	679	HMMER	PFAM: Elongation factor	PF00009	442.48	244	1344
ATP/CTP binding P-loop blastx.				1.8	Tu family (contains				
Piastx.2 ELONGATION FACTOR SpiP49411 EFTU_HU 89%					ATP/GTP binding P-loop)				1
TU, MITOCHONDRIAL MAN				blastx.2	ELONGATION FACTOR	sp[P49411 EFTU_HU	%68	112	1437
PRECURSOR (P43). PRECURSOR (P43). PRECURSOR (P43). PRECURSOR (P43). PRECURSOR (P43). PREAM: DEAD/DEAH PF00270 77					TU, MITOCHONDRIAL	MAN			
923110 630 HMMER PFAM: DEAD/DEAH PF00270 77					PRECURSOR (P43).				
2.1.1 box helicase blastx.2 CG4152 PROTEIN. splQ9Y134 Q9Y134 63% 61%	HLJDQ52	923110	630	HIMMER	PFAM: DEAD/DEAH	PF00270	177	405	785
1219455 631 blastx.2 CG4152 PROTEIN. sp Q9Y134 Q9Y134 61% 1219455 631 blastx.2 RNA helicase Gu - human pir PC6010 PC6010 66% 22% (fragment) 22% 1.8 DEAH box helicases pir 149731 149731 55% 1.8 DEAH box helicase - mouse pir 149731 149731 55% 1.8 DEAH box helicase pir 149731 55% 1.8 DEAH box helicase pir 149731 55% 1.8 DEAH box helicase pir 149731 55% 1.8 DEAH box helicase pir 149731 55%				2.1.1	box helicase				
1219455 631 blastx.2 RNA helicase Gu - human pir PC6010 PC6010 66% 22% (fragment) 22% 22% 1.8 DEAH box helicases pir 149731 149731 59% 1106635 632 blastx.2 RNA helicase - mouse pir 149731 149731 59% 1106635 632 blastx.2 RNA helicase - mouse pir 149731 149731 59% 1220017 633 blastx.14 RNA helicase [Mus 629.1 50% 1220017 633 blastx.2 Phorbolin I protein. 650 1.8 deoxycytidylate deaminases zinc-binding PF00383 24.31 1.8 deoxycytidylate deaminases zinc-binding PF00383 100% 1.8 deoxycytidylate deaminases zinc-binding HS271.1 protein 1 Phorbolin) Horbolin) Horbolin) Homo sapiens]				blastx.2	CG4152 PROTEIN.	sp Q9Y134 Q9Y134	63%	207	788
1219455 631 blastx.2 RNA helicase Gu - human pirPC6010 PC6010 66% 825697 893 HMMER PFAM: DEAD and PF00270 57.85 1.8 DEAH box helicase - mouse pir 149731 49731 59% 1.8 DEAH box helicase pir 149731 49731 59% 1.8 DEAH box helicase RF00270 159.42 1.8 DEAH box helicase RF00270 159.42 1.8 DEAH box helicase RF00270 159.42 1.8 DEAH box helicase RF00270 159.42 1.8 DEAH box helicase RF00270 159.42 1.8 DEAH box helicase RF00270 159.42 1.8 DEAH box helicase RF00270 159.42 1.8 DEAH box helicase RF00270 100% 1.8 DEAH box helicase RF00270 100% 1.8 deoxycytidylate deaminases zinc-binding PF00383 24.31 1.8 deoxycytidylate deaminases zinc-binding 45271.1 Protein 1 Phorbolin Phorbolin Honosapiens							61%	790	930
Regiment Regiment	HATAW40	1219455	631	blastx.2	RNA helicase Gu - human	pir/PC6010/PC6010	%99	470	2122
825697 893 HMMER PFAM: DEAD and PF00270 57.85 1.8					(fragment)		22%	233	556
1.8 DEAH box helicases pirl[49731 49731 59% 1106635 632 blastx.2 RNA helicase - mouse pirl[49731 49731 59% 1 908326 894 HMMER PFAM: DEAD and PF00270 159.42 1.8 DEAH box helicases [Mus gil407992 gb AAA53 69% 1220017 633 blastx.1 RNA helicase [Mus gil407992 gb AAA53 65% 2 933546 895 HMMER PFAM: Cytidine and G50 PF00383 24.31 2 933546 895 HMMER PFAM: Cytidine and G650 PF00383 24.31 1.8 dearninases zinc-binding region region PF002318) bK150C2.3 gil5102832 emb CAB 100% 1.8 At 277.1.1 protein 1 Phorbolin) HOUTATIVE novel 45271.11	HAJAW40	825697	893	HIMMER	PFAM: DEAD and	PF00270	57.85	490	702
7 908326 894 HMMER PFAM: DEAD and DEAD and BF00270 PF00270 159.42 7 908326 894 HMMER PFAM: DEAD and DEAD and BF00270 159.42 159.42 1.8 DEAH box helicases [Mus blastx.14 RNA helicase [Mus gil407992]gblAAA53 69% 69% 1220017 633 blastx.2 Phorbolin I protein. G50 50% 94% 12 933546 895 HMMER PFAM: Cytidine and Geoxycytidylate deaminases zinc-binding PF00383 24.31 1.8 deaxycytidylate deaminases zinc-binding 45271.1 PF00% Photbolin) Protein I Phorbolin) HMMER Phorbolin)				1.8	DEAH box helicases				
7 908326 894 HMMER PFAM: DEAD and 159.0270 159.42 1.8 DEAH box helicases 1.8 gil407992 gb AAA53 69% 1.220017 633 blastx.2 Phorbolin I protein. sp AAF86650 AAF86 94% 1220017 633 blastx.2 Phorbolin I protein. 650 100% 12 933546 895 HMMER PFAM: Cytidine and 650 PF00383 24.31 18 deoxycytidylate deaminases zinc-binding region region 100% 19astx.14 (AL022318) bK150C2.3 gi 5102832 emb CAB 100% 1000 protein 1 Phorbolin) HOUTATIVE novel 45271.1 1000 Homo sapiens] Homo sapiens] 1500.00	HATAZ67	1106635	632	blastx.2	RNA helicase - mouse	pir 149731 149731	29%	182	889
1.8 DEAH box helicases gil407992[gb AAA53] 69% blastx.14 RNA helicase [Mus musculus] 629.1[50% 1220017 633 blastx.2 Phorbolin I protein. sp AAF86650 AAF86 94% 2 933546 895 HMMER PFAM: Cytidine and deaminases zinc-binding PF00383 24.31 1.8 deoxycytidylate deaminases zinc-binding region 100% Plastx.14 (AL022318) bK150C2.3 gi 5102832 emb CAB 100% Protein 1 Phorbolin) [Homo sapiens] Homo sapiens]	HATAZ67	908326	894	HMMER	PFAM: DEAD and	PF00270	159.42	309	803
blastx.14 RNA helicase [Mus gil407992 gb AAA53 69% 1220017 633 blastx.2 Phorbolin I protein. sp AAF86650 AAF86 94% 1220017 633 blastx.2 Phorbolin I protein. sp AAF86650 AAF86 94% 1220017 633 blastx.2 Phorbolin I protein I Phorbolin) FFO0383 24.31 1.8 deoxycytidylate deaminases zinc-binding region region Protein I Phorbolin) 100% Protein I Phorbolin Phorb	-			1.8	DEAH box helicases				
1220017 633 blastx.2 Phorbolin I protein. sp AAF86650 AAF86 94% 100% 2 933546 895 HMMER PFAM: Cytidine and deaminases zinc-binding region region protein I Phorbolin) Homo sapiens] Homo sapiens] 100% 1				blastx.14	RNA helicase [Mus	gi 407992 gb AAA53	%69	177	788
1220017 633 blastx.2 Phorbolin I protein. sp AAF86650 AAF86 94% 650 100% 100% 1.8 deoxycytidylate deaminases zinc-binding region blastx.14 (AL022318) bK150C2.3 gi S102832 emb CAB 100% PUTATIVE novel 45271.1 Phorbolin) Homo sapiens]					musculus	629.1	20%	799	852
2 933546 895 HMMER PFAM: Cytidine and PF00383 24.31 1.8 deoxycytidylate deaminases zinc-binding region blastx.14 (AL022318) bK150C2.3 gi[5102832 emb CAB 100% 45271.1 protein 1 Phorbolin) [Homo sapiens]	HRITACO2	1220017	633	blastx.2	Phorbolin I protein.	sp AAF86650 AAF86	94%	66	620
933546 895 HMMER PFAM: Cytidine and deoxycytidylate PF00383 24.31 1.8 deoxycytidylate deaminases zinc-binding region 100% blastx.14 (AL022318) bK150C2.3 gi 5102832 emb CAB 100% protein 1 Phorbolin) protein 1 Phorbolin) Homo sapiens]			<u> </u>		•	650	100%	.611	926
deoxycytidylate deaminases zinc-binding region (AL022318) bK150C2.3 gi[5102832 emb CAB 45271.1 protein 1 Phorbolin) [Homo sapiens]	HBUAC02	933546	895	HMMER	PFAM: Cytidine and	PF00383	24.31	294	416
deaminases zinc-binding region gi[5102832 emb CAB (AL022318) bK150C2.3 gi[5102832 emb CAB (PUTATIVE novel protein 1 Phorbolin) 45271.1 [Homo sapiens] [Homo sapiens]				1.8	deoxycytidylate				
region (AL022318) bK150C2.3 gi[5102832 emb CAB 45271.1 protein 1 Phorbolin) [Homo sapiens]		^			deaminases zinc-binding				
(AL022318) bK150C2.3 gi 5102832 emb CAB (PUTATIVE novel 45271.1 protein 1 Phorbolin) [Homo sapiens]					region				
protein 1 Phorbolin) [Homo sapiens]				blastx.14	(AL022318) bK150C2.3 (PUTATIVE novel	gj5102832 emb CAB 45271.1	100%	57	599
[Homo sapiens]					protein 1 Phorbolin)				
	···				[Homo sapiens]				

177	40	177	177	40	615	10/9	333	915	904	092	243	803		350	347	400		967			403		403
43	2	37	37	5	94	618	28	163	863	221	63	767	70/	165	3	356		2			65		2
100%	%99	72.08	100%	%99	49%	21%	129.65	92%	71%	181.89	7020	71%	0/1/	85.33	%99	%98		93%			159.91		%98
sp BAA91606 BAA9	1606	PF00270	gi 2443870 gb AAB8	1544.1	sp Q9VHU1 Q9VHU		PF00270	659Y69J659Y69Jqs		PF00270	SERECTORIALIA A DA	81/3339031 80 AAD4	2/44.1 Ar 100012_1	PF00119	pir F59153 F59153			pir G65176 PWECA			PF00006		gi 42283 emb CAA23
CDNA FLJ10432 FIS,	CLONE NT2RP1000470, WEAKLY SIMILAR TO	PFAM: DEAD and DEAH how helicases	(AC002985) R27090 2	[Homo sapiens]	CG9630 PROTEIN.		PFAM: DEAD and DEAH box helicases	DEAD-BOX PROTEIN.		PFAM: DEAD and	DEATH DOX HEILCASES	(AF106019) DEAD-66x	protein [Homo sapiens]	PFAM: ATP synthase A chain	H+-transporting ATP	synthase (EC 3.6.1.34)	protein 6 - 1	H+-transporting ATP	synthase (EC 3.6.1.34)	alpna cnain - Eschencina coli	PFAM: ATP synthase	alpha and beta subunits	papA [Escherichia coli]
blastx.2		HMMER	blastx.14		blastx.2		HMMER	hlastx.2		HMMER	1.0	blastx.14		HMMER 1.8	blastx.2			blastx.2			HMMER	1.8	blastx.14
634		968			635		268	636)	868				637				638			899		
1117318		908245			1228148		772569	1713567	10000171	908303				587710				1152485			973667		
HCWEO14		HCWEQ14			HDPWH41		HDPWH41	HDOFH61	1007777011	нроены				HDTDD72				HFRBN02		-	HFRBN02		

		_			596.1	100%	406	651
					-	40%	574	633
HKAIH72	1107045	639	blastx.2	DNA POLYMERASE	sp 075417 DP0Q_H	%98	55	642
				THETA (EC 2.7.7.7) ONA POLYMERASE	OMAIN			
_				ETA).				
HKAIH72	761293	006	HMMER	PFAM: DNA polymerase	PF00476	86.06	55	522
			1.8	family A				
HMAAD90	1152487	640	blastx.2	NADH dehydrogenase	pir/JE0379/JE0379	100%	∞	250
				(ubiquinone) (EC 1.6.5.3)				
				chain NDUFA3 - human				
HMAAD90	963983	901	HMMER	PFAM: ATP:guanido	PF00217	932.7	1352	180
			2.1.1	phosphotransferase				
			blastx.14	sarcomeric mitochondrial	gi 338237 gb AAA60	100%	1199	171
			-0-	creatine kinase precursor	561.1	100%	1427	1392
				(EC 2.7.3.2) [Homo				
				sapiens]				
HMABQ71	1105540	641	blastx.2	DNA GYRASE	sp P06982 GYRB_E	%56	317	99
				SUBUNIT B (EC	COLI	%96	295	308
				5.99.1.3).		25%	70	2
HMABQ71	729831	902	HIMMER	PFAM: DNA	PF00204	128.8	210	407
			2.1.1	topoisomerase II (N-				-
				terminal region)			,	
HPJEV95	929723	903	HMMER	PFAM: ATP synthase A	PF00119	20.61	169	393
			1.8	chain				
HSKYR59	1219545	643	blastx.2	H+-transporting ATP	pir S22348 S22348	%06	639	181
			ALVE	synthase (EC 3.6.1.34)				
				delta chain precursor -				
				human				
HSKYR59	933750	904	HMMER	PFAM: ATP synthase,	PF00401	116.4	13	342

	2.1.1 Delt	Delta/Epsilon chain				
644 blastx.2		H+-transporting ATP synthase (EC 3.6.1.34)	pir S22348 S22348	%06	146	604
	delt hun	delta chain precursor - human				
905 HMMER 21.1	 	PFAM: ATP synthase, Delta/Epsilon chain	PF00401	148.1	206	586
blastx.14	 	H(+)-transporting ATP synthase [Homo sapiens]	gi 12586 emb CAA45 016.1	%06	146	604
645 blastx.2	DE.	DEAD-BOX PROTEIN ABSTRAKT	sp Q9UIV9 ABS_HU MAN	%96 %98	147	1442
906 HMMER		HOMOLOG. PFAM: DEAD and DEAH hox helicases	PF00270	92.34	142	387
646 HMMER 1.8	de de	PFAM: Cytidine and deoxycytidylate deaminases zinc-binding	PF00383	24.68	257	379
blastx.2	Phorbo	region Phorbolin I protein.	sp AAF86650 AAF86 650	94%	62 574	613 939
647 blastx.2	Syn Lipi pred	H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein P3 precursor, mitochondrial -	pir I38612 I38612	80%	107	421
907 HMMER	 	PFAM: ATP synthase subunit C	PF00137	38.73	312	422
blastx.14	syn ere	mitochondrial ATP synthase subunit 9 precursor [Homo sapiens]	gi 511450 gb AAA78 807.1	%08	108	422

HISGO19	1165320	648	blastx.2	CG9630 PROTEIN.	sp[Q9VHU1]Q9VHU	48%	559	1221
1	· · · · · · · · · · · · · · · · · · ·		·			46%	35	556
						46%	1205	1411
						25%	1413	1508
HUSGQ19	772568	806	HIMIMER	PFAM: DEAD and	PF00270	151.79	11	484
			1.0	DEATH DUA HEHICASES				
HUSZS75	1193982	649	blastx.2	CDNA FLJ11282 FIS,	sp BAA92106 BAA9	100%	738	459
				CLONE PLACE1009476,	2106	100%	31	153
				WEAKLY SIMILAR TO		100%	459	518
				1				
HUSZS75	908443	606	HMMER	PFAM: DEAD and	PF00270	93.7	505	792
•			1.8	DEAH box helicases				
			blastx.14	(AC004531) Gene with	gi 3337394 gb AAC2	%06	1046	1729
				similaity to DEAD box	7435.1	⁸⁸	319	780
				helicases [Homo sapiens]	-	100%	780	1115
				1		%16	112	234
						44%	1634	1687
HWBDR25	1174365	959	blastx.2	probable RNA helicase -	pir T08745 T08745	%16	12	1220
HWBDR25	659873	910	HMMER	PFAM: DEAD and	PF00270	170.59	24	416
			1.8	DEAH box helicases				
HBGSS51	954855	651	HMMER	PFAM: Cytidine and	PF00383	34	99	173
			2.1.1	deoxycytidylate			_	
				deaminase zinc-binding				
				region				
			blastx.14	(AL117202) predicted	gi 5832838 emb CAB	%95	75	206
				using Genefinder;	55073.1	41%	216	266
				preniminary i				

Table 2 further characterizes certain encoded polypeptides of the invention, by providing the results of comparisons to protein and protein family databases. The first column provides a unique clone identifier, "Clone ID NO:", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" which allows correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:", for the contig polynucleotide sequences. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. The fifth column provides a description of the PFAM/NR hit identified by each analysis. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, score/percent identity, provides a quality score or the percent identity, of the hit disclosed in column five. Comparisons were made between polypeptides encoded by polynucleotides of the invention and a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM"), as described below.

The NR database, which comprises the NBRF PIR database, the NCBI GenPept [52] database, and the SIB SwissProt and TrEMBL databases, was made non-redundant using the computer program nrdb2 (Warren Gish, Washington University in Saint Louis). Each of the polynucleotides shown in Table 1A, column 3 (e.g., SEQ ID NO:X or the 'Query' sequence) was used to search against the NR database. The computer program BLASTX was used to compare a 6-frame translation of the Query sequence to the NR database (for information about the BLASTX algorithm please see Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993). A description of the sequence that is most similar to the Query sequence (the highest scoring 'Subject') is shown in column five of Table 2 and the database accession number for that sequence is provided in column six. The highest scoring 'Subject' is reported in Table 2 if (a) the estimated probability that the match occurred by chance alone is less than 1.0e-07, and (b) the match was not to a known repetitive element. BLASTX returns alignments of short polypeptide segments of the Query and Subject sequences which share a high degree of similarity; these segments are known as High-Scoring Segment Pairs or HSPs. Table 2 reports the degree of similarity between the Ouery and the Subject for each HSP as a percent identity in Column 7. The percent identity is determined by dividing the number of exact matches between the two aligned sequences in the HSP, dividing by the number of Query amino acids in the HSP

and multiplying by 100. The polynucleotides of SEQ ID NO:X which encode the polypeptide sequence that generates an HSP are delineated by columns 8 and 9 of Table 2.

[53] The PFAM database, PFAM version 2.1, (Sonnhammer et al., Nucl. Acids Res., 26:320-322, 1998)) consists of a series of multiple sequence alignments; one alignment for each protein family. Each multiple sequence alignment is converted into a probability model called a Hidden Markov Model, or HMM, that represents the position-specific variation among the sequences that make up the multiple sequence alignment (see, e.g., Durbin et al., Biological sequence analysis: probabilistic models of proteins and nucleic acids, Cambridge University Press, 1998 for the theory of HMMs). The program HMMER version 1.8 (Sean Eddy, Washington University in Saint Louis) was used to compare the predicted protein sequence for each Query sequence (SEQ ID NO:Y in Table 1A) to each of the HMMs derived from PFAM version 2.1. A HMM derived from PFAM version 2.1 was said to be a significant match to a polypeptide of the invention if the score returned by HMMER 1.8 was greater than 0.8 times the HMMER 1.8 score obtained with the most distantly related known member of that protein family. The description of the PFAM family which shares a significant match with a polypeptide of the invention is listed in column 5 of Table 2, and the database accession number of the PFAM hit is provided in column 6. Column 7 provides the score returned by HMMER version 1.8 for the alignment. Columns 8 and 9 delineate the polynucleotides of SEQ ID NO:X which encode the polypeptide sequence which show a significant match to a PFAM protein family.

[54] As mentioned, columns 8 and 9 in Table 2, "NT From" and "NT To", delineate the polynucleotides of "SEQ ID NO;X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth column. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the polynucleotides of SEQ ID NO:X delineated in columns 8 and 9 of Table 2. Also provided are polynucleotides encoding such proteins, and the complementary strand thereto.

[55] The nucleotide sequence SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, the nucleotide sequences of SEQ ID NO:X are useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in Clone ID NO:Z. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling

immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to these polypeptides, or fragments thereof, and/or to the polypeptides encoded by the cDNA clones identified in, for example, Table 1A.

- Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).
- [57] Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, and a predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing cDNA Clone ID NO:Z (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, and having depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.
- [58] The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

RACE Protocol For Recovery of Full-Length Genes

[59] Partial cDNA clones can be made full-length by utilizing the rapid amplification of cDNA ends (RACE) procedure described in Frohman, M.A., et al., Proc. Nat'l. Acad.

Sci. USA, 85:8998-9002 (1988). A cDNA clone missing either the 5' or 3' end can be reconstructed to include the absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start codon of translation, therefor. The following briefly describes a modification of this original 5' RACE procedure. Poly A+ or total RNA is reverse transcribed with Superscript II (Gibco/BRL) and an antisense or complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT primer containing three adjacent restriction sites (XhoI, SalI and ClaI) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide-agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or SalI, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with the putatively identified homologue and overlap with the partial cDNA clone. Similar methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-stranded ligation to single-stranded cDNA), developed by Dumas et al., Nucleic Acids Res., 19:5227-32 (1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dA-tailing reaction which results in a polyT stretch that is difficult to sequence past.

[61] An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is

synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a symmetric PCR reaction is performed with a nested cDNA-specific antisense primer and the plasmid-anchored primer.

RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes

[62] Once a gene of interest is identified, several methods are available for the identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3' RACE. While the full length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the existing sequence information from the original cDNA to generate the missing information. A method similar to 5' RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., Nucleic Acids Res., 21(7):1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcript and a primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A RNA may be used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase if used is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant gene.

[63] The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, and receiving ATCC designation numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, Table 6, or Table 7) is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as described, for example, in Table 7. These deposits are referred to as "the deposits" herein. The tissues from which some of the clones were derived are listed in Table 7, and the vector in which the corresponding cDNA is contained is also indicated in Table 7. The deposited material includes cDNA clones corresponding to SEQ ID NO:X described, for example, in Table 1A (Clone ID NO:Z). A clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X, may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Furthermore, although the sequence listing may in some instances list only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to sequence the DNA included in a clone contained in the ATCC Deposits by use of a sequence (or portion thereof) described in, for example Tables 1Aor 2 by procedures hereinafter further described, and others apparent to those skilled in the art.

- [64] Also provided in Table 7 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.
- [65] Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into E. coli strain XL-1 Blue, also available from Stratagene.

Vectors pSport1, pCMVSport 1.0, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus 15:59-* (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res. 16:*9677-9686 (1988) and Mead, D. *et al.*, *Bio/Technology 9:* (1991).

- [67] The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the deposited clone (Clone ID NO:Z). The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.
- Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X or the complement thereof, polypeptides encoded by genes corresponding to SEQ ID NO:X or the complement thereof, and/or the cDNA contained in Clone ID NO:Z, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.
- [69] The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.
- [70] The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often

advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

[72] The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA sequence contained in Clone ID NO:Z. The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEO ID NO:X or a complement thereof, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or the polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or a polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, a nucleic acid sequence encoding a polypeptide encoded by the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA contained in Clone ID NO:Z.

Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in Table 1B column 6, or any

combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[74] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated

in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

Further, representative examples of polynucleotides of the invention comprise, or [75] alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (See Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[76] Moreover, representative examples of polynucleotides of the invention comprise. or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. In preferred embodiments, the polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, wherein sequentially delineated sequences in the table (i.e. corresponding to those exons located closest to each other) are directly contiguous in a 5' to 3' orientation. In further embodiments, above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1B, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same Clone ID NO:Z. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[79] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same row of column 6 of Table 1B. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[80] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[81] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X are directly contiguous Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent

hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids; other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[82] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[83] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides, are also encompassed by the invention.

In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization

conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[85] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same Clone ID NO:Z (see Table 1B, column 1) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one sequence in column 6 corresponding to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[87] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same row are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B is directly contiguous with the 5' 10 polynucleotides of the next

sequential exon delineated in Table 1B, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

Many polynucleotide sequences, such as EST sequences, are publicly available [88] and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. Accordingly, for each contig sequence (SEQ ID NO:X) listed in the fourth column of Table 1A, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, b is an integer of 15 to the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. More specifically, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a and b are integers as defined in columns 4 and 5, respectively, of Table 3. In specific embodiments, the polynucleotides of the invention do not consist of at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. as disclosed in column 6 of Table 3 (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone). In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example. All references available through these accessions are hereby incorporated by reference in their entirety.

TABLE 3

	SEQ				
	ID]	ECT D		
Clone ID	NO:		Range of a	sclaimer Range of b	
NO: Z	X	Contig ID:			Accession #'s
HHMMC14	11	1152250	1 - 1314	15 - 1328	AI086374, AI985881, AI760724,
	1				AW025363, AI744911, AI417334,
		1			AI608898, AI185630, AI086397,
	ĺ	·			AI419401, AI983536, AW250705,
]		[AA657972, W28944, AA767300,
					AA706825, AI587185, AI189408,
			1		AW248699, AW073190, AI347314,
	1				AI524186, AA563745, AA495799,
			1		AI168297, AI310528, AW130176,
			1		AA838407, AI955019, AI346558,
		İ	-		AI356497, AI028668, AA917828,
					AW246849, AI140292, AI084924,
Ì			}		AA232967, AI148985, AI678784,
	.				AI281328, AA948694, AI082557,
		,	ł		AI150722, AI276605, AI014882,
ļ			ļ		AI803268, AW169494, AI333698,
					AI333302, AA253369, AI740611,
					AI831634, AA670367, AI082804,
ļ			i		AI080366, AA777091, AI816955,
				i	AI753298, AW028800, AI679052,
ľ	i	ĺ	i		AA764739, AI215157, AI393800,
					AA148919, AW404750, W49510,
		i	l		AI087262, AI197944, AI089710, T70527,
	1		1		AA253492, N54782, AI344641, AI460108,
	ľ		ŀ		AI933303, AA315786, W79013, AI539484,
. [İ		T79608, AA076080, AI971904, AA300208,
į	l		1		AI290314, AA677875, AI347377,
ľ					AI183485, AA743340, AA775359, D63259,
					AA989095, AA507572, AA705697,
	1	j	ı		W16716, R83908, AI362504, AA749447,
	i	ļ	}		AA708333, AI857590, W46838,
	ĺ	İ			AW069333, AA495736, AA410264,
1	Į.		·		H57844, AA625770, N79535, AI262439,
1	f				T68602, N90776, AA865920, W19200,
	l			i	AA306173, AA865906, AA099528,
		İ			AW192370, W80405, AA234363,
	1	1		1	AA128388, AW249131, T30208, R83907,
1.	.	1	- 1	i	AA194982, N75707, AA362705, AI221840,
			l		AA458624, AI921358, AA194997,
1	Ì	Ì			AA808409, AA588355, AA887944,
}		1	1	j	AI264098, AA234413, C17057, W49511,
		i	-	Ì	N90242, AI245717, T16103, AI127393,
ļ]	ł	j	i	AA255797, AA933878, AA557707,
j		ļ	ļ	ļ	AA641364, AA256690, H63263, T34009,
l		[İ	{	H38215, AA480658, AI041628, AA148891,
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		1			AI368525, AA358466, N49510, AA336108,
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	1				AI269350, H44001, AI080399, T81384,
	ľ				T68683, AI990425, T72355, N75325,
					AA199911, AA233135, AA846765,

1					AI352057, AI954908, AI422513,
	ļ				AI434527, AA887052, AA406584,
Í		(1	AA359371, F37868, W04776, AI311094,
ì	1	1	j	1	H37992, T79693, R82477, AI473295,
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ļ]	1	}		AA552356, H59969, AI864371, AA479548,
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		1	ł		AA805180, AA429337, R36837, AI241215,
}					T41059, C20939, AA346761, AA173883,
!	1	{			AA248560, AA808574, AA605086,
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	.	[1	D63259, AA255797, AW249131, C17057,
}	ŀ			1	AI041628, AA148891, AA377553, T81384,
1 '			1	l	T72836, T68683, T72355, AA309101,
<u>}</u> .			1	l	AA358466, AA359371, W04776,
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			j	1	AA495736, AF134895, AF146018,
IDICOVIO	1.4	1150054	1 1146	l	AF113251, and AF146689.
HNGOW33	14	1152254	1 - 1146	15 - 1160	AI526183, A38246, AR029496, A11542,
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HT4GD03	15	1103896	1 - 1185	15 - 1199	AI468008, AI492094, AI970413,
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}		·]		AI972753, AI964003, AI656960,
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]					AI198343, N93695, AI911538, AA766826,
					W21033, AI814342, AI991685, AA888820,
}				!	AJ366738, AW001123, C14331, C14429,
]		D59859, AW177440, T03269, C14389,
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ļ				1	D58283, D80022, D80166, D80195,
ſ			[
J	1		'		D80193, D59927, D59467, D51423,
	ſ				D59619, D80210, D80391, D80164,
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	ļ				D80043, D59787, D80227, D59502,
	ĺ	'			AW378532, D81030, AW352117, D80212,
)			1	D80196, D80219, C15076, D80269,
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					AW375406, AW378534, AW377672,
					AW179023, AW178905, AA514188,
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					AW378528, AW179019, AW179024,
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		İ		·	AW360834, AA514186, D80133,
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	Ì	1			AW179004, C05695, D80439, D80268,
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					AA285331, C14227, AW178983,
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	1	1			AI984679, W52097, AI281829, AA236375,
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		1			N63941, N58535, AA367722, AL042537,
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ļ					AA833560, AW351523, AL119457,
		ļ	}	ļ	AW392670, Z99396, AL119324, U46351,
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ļ			ì		AL119401, AL119522, AL119439,
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	'				AL039851, AL042965, AL042975,
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HEFFB39	20	946170	1 - 1601	15 - 1615	AI631883, AI767614, AA018867, R56792,
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	<u> </u>				R56793, Z38315, and Z42023.
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ł	ľ				AA514184, AI535959, AI535686,
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HE9DG38	22	1181748	1 - 1442	15 - 1456	AA911739, AI424010, AW082869,
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]			İ		N55218, AA312035, N56305, R13983,
1		1			A1792322, AI791644, and H28118.
HGBAT24	23	1024746	1 - 406	15 - 420	D57159.
HTDAF92	24	1181747	1 - 1147	15 - 1161	AA312035, AA911739, AI791644,
IIIDAI 72	~	1101/4/	1-11-7/	13-1101	AI792322, R13983, AI424010, AW082869,
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	1	ļ			N56305, AI422406, H30676, F06133,
TIADOTTO	25	669405	1 205	15 300	R13816, R37777, R13678, and AI732836.
HAPSI19	25	668405	1 - 385	15 - 399	AI887474, AI065167, AI114842,
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			AA468090, AA134092, AA469455,
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			AA194499, AA879244, AA178872,
			AA424930, AA192816, AA524630,
,			C16951, AA650350, AA206277, AI525589,
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			AA194687, AA112861, AI525178,
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			AI720611, AA522594, C17424, AI720582,
			AA132126, AA194546, AA737156,
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		İ	AA192574, AI557370, AA192670,
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			AA478982, AA213947, AA745378,
			AA079046, AI601133, AI749789,
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TTODA TIE	40	1001626	1 - 622	15 - 636	
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PCT/US01/01239

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PCT/US01/01239

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PCT/US01/01239

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			1		X78627, AF124396, U95114, AL137530,
					AF172400, AF106697, AL122100, and
					AF184965.
НСЕРЈ44	147	1157810	1 - 899	15 - 913	AA326315, F11730, and U15976.
HCWCM65	148	1105668	1 - 699	15 - 713	
HDQDY52	149	1182322	1 - 771	15 - 785	AW015554, AW139739, AA284952,
			1		AI478494, AA918422, AL049709, and
HEET 100	4.50	1000110	1 1000		AF216873.
HEEAA32	150	1203140	1 - 1920	15 - 1934	AI733019, AI821967, AI401824,
		ļ		j	AI305817, AI248775, AI791417, N63067,
					AA769662, AI636297, AI436700,
			1		AI373787, AI279773, AI823325, AI913400, AI431755, AW271322,
			1		AA873330, AW006890, AI433320,
			-		AW027962, and AW772149.
HEGAN70	151	839719	1 - 891	15 - 905	AA995279, M78884, and AB023151.
HFKMF42	152	1104119	1 - 1544	15 - 1558	AW025904, AW008529, AI680826,
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			į		AI015927, AA805175, AA251134,
		· ·	1	Ţ	AA310596, AA603773, AA516361,
					F08785, AA953720, AI701937, AA852503,
·			1	1	AA687875, AI873898, AA251198,
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}			1	ł	AW081255, AI473598, AI468872,
1			:		AI699011, AI866608, AI758528,
1					AW088899, AI273843, AI446373,
1				j	AI343059, AI349933, AI932638,
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				1	AI491783, AL040241, AI474107,
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ł	1		1		D14859.
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		1.	İ		Z44504, AA091214, AI250518, D86980,
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					AA001398, AA601230, AA493931,
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	1	ļ			AI333009, AF006747, AA878505, R40908,
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			ļ	-	R13392, AI589503, AW149318,
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HODSEZZ	300	11212/1	1 - 649	15 - 663	AI806796, AA740715, AA205032,
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HDPFM16	302	1193042	1 - 2116	15 - 2130	AF118067, and AW589858. AI347260, AI056270, W87850, AI992086,
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			1		AC005792, AC009399, AC004103, and
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HTPIL46	307	1196787	1 - 2474	15 - 2488	AW137063, AI473912, AA044687,
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HHFGD45 HNHEB44 HMACX92	332 333 334	1151161 1161293 1151497	1 - 902 1 - 697 1 - 1350	15 - 916 15 - 711 15 - 1364	AW250611, AA100409, AA179613, T74720, AI302489, AA316917, N25590, AW410441, AA836520, R95063, N34189, F12758, AW410323, AW264652, AA888873, AA620477, W19483, AI564941, AW410275, AA131652, H08125, AI583139, AA321590, H96758, H22827, AA948010, AI268613, T29731, T82107, AA377688, AI865572, AA353258, AA323383, T76964, H22828, AA747352, AA165534, H96748, AA328132, AA348084, T77128, AI142430, AA888553, AA361530, AI915153, AI138694, AA317532, AW075505, AA243310, AA810043, AA233215, AW411491, AA219520, AI383174, AA356005, F10366, R34798, AA328880, AA179614, AA864537, AI702255, N87314, AW410237, T15483, N90299, AI144004, AA243309, AA369495, AA910240, AI313297, AI557895, AA630033, AA102177, W44661, AW296682, AA693453, AW410276, AA131470, AA716519, AA235484, N58211, D11830, H39749, AW410936, AA454097, AA187947, L11932, X91902, U23143, Z62251, and Y12331.
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HMCBN45	242	927125	1 - 1033	15 - 1047	AI763246, AI142222, AA243784,
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HBXAW47	348	771624	1 - 668	15 - 682	AA028190, AI953574, AI738595,
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1					AF101446, AF077202, AE031723, and
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HBMXQ90	388	922114	1 - 449	15 - 463	AA149171, AI984559, AA934684,
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HOEJV72	389	930778	1 - 833	15 - 847	AI378980, AA354580, AW401983,
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HUKFO68	392	951652	1 - 1100	ł	
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HFXJW08	393	959204	1 - 676	15 - 690	AC026761, AC026761, and AC009091.
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TIESTO51	393	403207	1 32.		AA309852, and AA399121.
HTPDU31	396	503077	1 - 352	15 - 366	R20319, AA322955, and Z83844.
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HMHBS90	398	574062	1 - 604	15 - 618	AW381702, AW381701, AA677535,
HMHB230	390	374002	1 - 004	13 010	AA223851, W67779, AA429201,
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HNGJQ15	403	-660310	1 - 354	15 - 308	AC017028.
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HSIAC23	407	679292	1 - 446	15 - 460	H14396, R19960, F11251, R12516, AA376792, AF095286, AF019638, and
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HSLFL74	408	685897	1 - 1332	15 - 1346	
HSDJD53	409	698259	1 - 611	15 - 625	700050 NEEDO POODES 1 A A 221022
HCEBF33	410	702955	1 - 897	15 - 911	R20250, N57610, R20853, and AA321932.
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HHGDG42	417	724795	1 - 346	15 - 360	W68048, AA676817, AI248718, AI356839,
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HMTMF31	418	731302	1 - 412	15 - 426	AI908495, AI908497, H06611, Z44955,
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HNDAG60	420	. 751953	1 - 433	15 - 447	AI909320, AA211037, AL135260,
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HSLDS79	421	753247	1 - 1643	15 - 1657	T00000 10000000 110000000
HFBCQ61	422	769102	1 - 232	15 - 246	T05065, AC022886, and AC022886.
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HLDQV23	424	788957	1 - 492	15 - 506	W67622, R15231, H29786, Z45968,
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HSUME31	426	812373	1 - 559	15 - 573	AA380193, AA805469, AW410817,
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HUSHB56	427	815819	1 - 400	15 - 414	
	428	824708	1 - 1730	15 - 1744	
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HKACD80	430	837698	1 - 681	15 - 695	AW239293, R67182, R57498, R38144, and

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HEEDIZ 40	431	837782	1 - 615	15 - 629	U46280, and R20122.
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HE9SS77	432	838043	1 - /12	13-720	AB029000.
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HRADE27	444	867195	1 - 535	15 - 549	AA809467, N50856, and D87455.
HTXQR10	445	869137	1 - 553	15 - 567	AA308909, H39234, H86515, H86668, and AA053340.
HEQCB27	446	871062	1 - 414	15 - 428	
HE8AM04	447	871156	1 - 506	15 - 520	AA378845, AA332652, AA331633, AL031774, AL031774, AL031774, AL138825, AL138825, and AL138825.
HSLHT48	448	871996	1 - 832	15 - 846	AC024580, AC020865, and AC026761.
HS2SH70	449	875870	1 - 1002	15 - 1016	AI159768, AA311553, AA313233, AA336308, AI916593, F08346, AW269297, AA376331, AI651236, AI968341, AA374806, AI650685, AA781008, T99283, and AL133500.
HAOAE45	450	876157	1 - 460	15 - 474	AA214170, AA313857, and Z98048.
HELBA42	451	878549	1 - 1000	15 - 1014	R54355, AA311209, AA357633, AA471387, AL050269, AC016888, and AC016888.
HSPBB15	452	878791	1 - 943	15 - 957	AI741739, AI034449, AW167538, AW449121, AW450678, AI025866, AA052927, AA324019, AI914219, AW449405, H84106, H84348, AA954604, AA772473, AA862600, and X94769.
HTAFF91	453	879399	1 - 417	15 - 431	AL353658, AL353658, AL353658, AL121829, AL121829, and AL121829.
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HGBCU40	455	880328	1 - 612	15 - 626	AA160076, and AA358669.
HE9PR39	456	882939	1 - 658	15 - 672	AA205757, and Y11342.
HTEAF36	457	839516	1 - 416	15 - 430	W58006, AI668926, W58089, AI831877,
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HMUBI13	488	937820	1 - 970	15 - 984	AW160967, AA211700, AI341467,
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	1				AA555145, AI345415, AI345688,
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HFRAU96	539	527840	1 - 539	15 - 553	T56179.
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HSLFF79	542	609838	1 - 898	15 - 912	ACOUSTOS, and ACOUSTOS.
HKTAB71	543	661483	1 - 736	15 - 750	AA777511, AA203750, AI469206,
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Harrier		670000	<u> </u>	15 540	AA894649, AF111858, and AL023806.
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HNHHW82	545	684342	1 - 270	15 - 284	AC074221, AC074221, AC020884, and
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HTLBH79	549	774422	1 - 560	15 - 574	AI927735, AW081044, AA662961,
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HSDKI89	551	786812	1 - 509	15 - 523	AC012620.
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IIWOA341	254	827310	1-3/3	13-30/	D42047.
HTXOH20	555	837509	1 - 636	15 - 650	AA429144, W27414, T65501, R13762,
HIXOHZU	ددد	837309	1 - 030	13 - 030	
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HSLFG13	556	847314	1 - 693	15 - 707	AC008792.
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HOVEB13	575	917564	1 - 1360	15 - 1374	AL119443, AW363220, AL119335, AL119483, U46351, AL119363, AL119496, AL119401, AL119355, AL119341, AL119399, U46350, AL119418, AL119439, U46349, U46341, U46347, AL119444, AL134524, AL037205, AL134536, U46346, AL134527, AI142137, AL134525, U46345, AL134518, AL134528, AL134538, Z98258, AR060234, AR066494, A81671, AR069079, AB026436, and AR054110.
HOVEB13	575	917564	1 - 1360	15 - 1374	AL119443, AW363220, AL119335, AL119483, U46351, AL119363, AL119496, AL119401, AL119355, AL119341, AL119399, U46350, AL119418, AL119439, U46349, U46341, U46347, AL119444, AL134524, AL037205, AL134536, U46346, AL134527, AI142137, AL134525, U46345, AL134518, AL134528, AL134538, Z98258, AR060234, AR066494, A81671, AR069079, AB026436, and AR054110. AA928779, AI685200, AA576884,
HOVEB13	575	917564	1 - 1360	15 - 1374	AL119443, AW363220, AL119335, AL119483, U46351, AL119363, AL119496, AL119401, AL119355, AL119341, AL119399, U46350, AL119418, AL119439, U46349, U46341, U46347, AL119444, AL134524, AL037205, AL134536, U46346, AL134527, AI142137, AL134525, U46345, AL134518, AL134528, AL134538, Z98258, AR060234, AR066494, A81671, AR069079, AB026436, and AR054110. AA928779, AI685200, AA576884, AI218215, AI809292, AI355487,
HOVEB13	575	917564	1 - 1360	15 - 1374	AL119443, AW363220, AL119335, AL119483, U46351, AL119363, AL119496, AL119401, AL119355, AL119341, AL119399, U46350, AL119418, AL119439, U46349, U46341, U46347, AL119444, AL134524, AL037205, AL134536, U46346, AL134527, AI142137, AL134525, U46345, AL134518, AL134528, AL134538, Z98258, AR060234, AR066494, A81671, AR069079, AB026436, and AR054110. AA928779, A1685200, AA576884, AI218215, A1809292, AI355487, AW082223, AW263592, AA424504,
HOVEB13	575	917564	1 - 1360	15 - 1374	AL119443, AW363220, AL119335, AL119483, U46351, AL119363, AL119496, AL119401, AL119355, AL119341, AL119399, U46350, AL119418, AL119439, U46349, U46341, U46347, AL119444, AL134524, AL037205, AL134536, U46346, AL134527, AI142137, AL134525, U46345, AL134518, AL134528, AL134538, Z98258, AR060234, AR066494, A81671, AR069079, AB026436, and AR054110. AA928779, AI685200, AA576884, AI218215, AI809292, AI355487, AW082223, AW263592, AA424504, AW152614, AI265774, AW070728,

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ļ	1	1	1	ļ	Y10655, L19437, L30117, X52128,
1		1	1		AF153205, AF111849, X92070, Y10080,
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	1				AL133665, AF026816, I41145, AF067728,
	1				E04233, AL080159, AR000496, and
	l	<u>L</u>	}	l	U39656.
HE8UB94	576	920288	1 - 547	15 - 561	AL039567, AA088498, AA424424,
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HTHDJ23	577	921274	1 - 1727	15 - 1741	AA251720, AA319062, AI057495,
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HWHPB72	578	922580	1 - 766	15 - 780	AL036002, F03069, AA449870, F04459.
IIWIN D/2	378	922360	1 - 700	13 - 780	
İ	-		İ	ł	F04460, T83997, AA083638, W56855,
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HSQFX64	579	922581	1 - 407	15 - 421	AI807806, AA773032, AA666091,
ĺ	(				AI478904, AL049697, AL049697,
	1	<u> </u>			AL049697, and AL049697.
HDABB84	580	922582	1 - 1810	15 - 1824	AI807806, AI016336, AI761537,
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			1		W56855, F03069, W77737, T79040,
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HLHFN83	581	924110	1 - 662	15 - 676	AI765848, AI435448, AI458176,
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HCEEC58	584	933866	1 - 314	15 - 328	D42047.
HSYAD06	585	935334	1 - 751		<del> </del>
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HEGAU68	588	950009	1 - 558	15 - 572	AA057228, H85626, H39014, H37972,
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HNGKH38	589	951032	1 - 237	15 - 251	AI963473, AC019122, AC019122, and
			] -	}	AC019122.
HNHNN26	590	952398	1 - 392	15 - 406	AC078913, AC074334, AC074334, and
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HTEHP64	591	953791	1 - 488	15 - 502	AI962178, AW301662, AA906865,
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HMIAO78	592	953793	1 - 666	15 - 680	AI962178, AW301662, AA906865,
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HFPCN94	593	955009	1 - 1460	15 - 1474	AI830691, AI948511, AI357436,
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	1			1	AI417903, AW165982, AW271819,
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HSLHV08	594	958582	1 - 153	15 - 167	AC074221, AC022123, and AC055703.
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HPDVW40	595	961039	1 - 951	15 - 965	AI948584, AI678666, AI765219,
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1	1				AI003925, AI004690, AA194383,
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					AI144132, AW203978, AI813349,
		i			AI624882, AI767866, AI142908,
					AI290470, AI208243, H83611, H82735,
			į		AA436020, AA507760, AI208044, N89963,
ĺ					F32992, AI865963, AW205754, R23657,
•					F24958, AA112966, AA436128, F18071,
					Z25302, T30841, C04894, R24601, F29302,
	ļ				
	i				T30825, R24502, C00537, AW297508,
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HEMFC70	596	961963	1 - 1564	15 - 1578	AI674223, AW372210, AA600053,
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	ļ				AA280511, AF151828, AF147717,
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HLDOO20	597	910371	1 - 145	15 - 159	AI432644, AI623302, AI432653,
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HSENS89	600	964527	1 - 1039	15 - 1053	W52878, R10513, R17310, AL117452, and
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HNTAF77	601	966190	1 - 505	15 - 519	AI436205, AI280203, AA479713,
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ļ	1			1	AI557278.
HBIOV48	602	967566	1 - 523	15 - 537	T87573, and AL049709.
HBGMN45	603	967744	1 - 696	15 - 710	AC022123.
HBXCE20	604	970889	1 - 880	15 - 894	
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HKGDQ60	606	863330	1 - 756	15 - 770	AI929390, F00197, Z24927, AA019708,
		·	<u> </u>		AC002400, and Z59200.
HSDKF67	607	933059	1 - 456	15 - 470	AC020885.
HSLFT94	608	603023	1 - 416	15 - 430	
HTJMD06	609	837603	1 - 482	15 - 496	AB002346, AF039945, AF041860,
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HNTBH68	610	851274	1 - 569	15 - 583	AW157233, Z43649, C15376, and R20382.
HMEKO39	611	863507	1 - 669	15 - 683	
HAABH11	612	965473	1 - 685	15 - 699	AA418447, H83353, H85525, and
ĺ				1	AA759336.
HUVFZ43	613	910860	1 - 1436	15 - 1450	AL121363, AI569727, AL121364,
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HHEJR23	616	919082	1 - 850	15 - 864	AI440338, AA868192, AI808409,
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	618	729217		15 - 349	R88881, and AI863797.
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			ł		AA664029, AW366681, AI318079,
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Į.		l .	i	1	AA148676, AA094905, AA148677,
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		}			AI275830, AI242246, D42084, and
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HFXHD52	626	490721		15 - 626	L48842, and X55499.
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HCWEO14	634	1117318	1 - 355	15 - 369	R16298, AA488261, R15246, AA325932,
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HDQEH61	636	1213567	1 - 902		AA232431, AF171063, AL049557,

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HFRBN02	638	1152485	1 - 975	15 - 989 15 - 1546	
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	1				AA694117, AA088451, AI749360,
1	1	Ĭ	į.		AI088643, AA576203, AI718389, F20628,
	1				AA287074, F26081, N26049, D20716,
	1				AA721698, AA284531, AW273893,
	1			1	N53859, AI469668, AA502645, AI033719,
	1			ļ	AI420366, F20597, H98101, AI189806,
ŀ	1				A1420300, F20397, F190101, A1103000,
	j i				N34652, AI636826, AA064910, AA917751,
1	1		1	ŀ	R98575, AA575937, AA421366,
		1	}	ì	AA935737, W72160, AI186260, N32788,
				ľ	AA477331, AA158600, N31599,
	ł		ì	1	AA401100, AI193952, W42983, AI340972,
1			1	ļ	C03853, AA479750, AA564885, AI034254,
		(	1	1	AI358074, AA992042, AA491987, H70695,
1	1			1	N20951, AI128894, AA654495, R80833,
	Į.				N20951, A1128894, AA034495, R60055,
I	Í	4			AI333433, AA576225, AA421285,
1				1	AA065189, W02947, AA782455, R92244,
	i				AI766437, AA582561, AA782733,
· ·					AI784600, AA158981, AA035404,
	1	ļ		1	AA158621, W00676, H82450, AW191872,
1	1				AI301326, AI749232, AA484185, H23877,
	ŀ			İ	AA890312, AI359315, AA112059, N73359,
İ		1	1		AA690512, A£539313, AA112033, 1173333,
1				ſ	AA669504, R98056, AI073522, AI129443,
		1	1		N27821, AI689201, AA322157, T29641,
1	ŀ	1	ł	1	H78773, W74603, AA197117, AW004770,
{	1				AI581927, AA010122, AA035403,
			1	1	AA149110, H47164, R98576, AA664772,
	1		1	1	AA187062, N49759, R98296, R93304,
	1		1	1	AW273793, W42984, AW299631, H78692,
1	-	1		1	AWZ/5/95, W4Z904, AWZ99051, 11/8092,
	1	Į.	1	1	AA340920, H47080, AA375173,
1		1		1	AA121112, N88492, H91239, H65548,
1	1		1	ļ	F33675, N91473, F36132, AA065188,
1		1	1		AA010121, H91185, AA629726, N69009,
1	1		1	}	AA135829, AA345017, N42658, F36640,
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## TABLE 4

Code	Description	Tissue	Organ	Cell Line	Disease	Vector
AR022	a Heart	a Heart				
AR023	a Liver	a Liver				
AR024	a manunary gland	a mammary gland				
AR025	a Prostate	a Prostate				
AR026	a small intestine	a small intestine				
AR027	a Stomach	a Stomach				
AR028	Blood B cells	Blood B cells				
AR029	Blood B cells activated	Blood B cells				
		activated				
AR030	Blood B cells resting	Blood B cells resting				
AR031	Blood T cells activated	Blood T cells activated				
1.0000	71 17 11				<del></del>	
AR032	Blood T cells resting	Blood T cells resting			<del></del>	<del></del>
AR033	brain	brain	<b></b>		<del> </del>	<del></del>
AR034	breast	breast			ļ	<u> </u>
AR035	breast cancer	breast cancer			ļ	
AR036	Cell Line CAOV3	Cell Line CAOV3	ļ		ļ	
AR037	cell line PA-1	cell line PA-1			ļ	<u> </u>
AR038	cell line transformed	cell line transformed			ļ	
AR039	colon	colon			ļ	
AR040	colon (9808co65R)	colon (9808co65R)				
AR041	colon (9809co15)	colon (9809co15)			ļ	<u> </u>
AR042	colon cancer	colon cancer	<u> </u>			
AR043	colon cancer (9808co64R)	colon cancer (9808co64R)				
AR044	colon cancer 9809co14	colon cancer 9809co14				
AR045	corn clone 5	corn clone 5				
AR046	corn clone 6	corn clone 6				
AR047	corn clone2	corn clone2	1			
AR048	corn clone3	corn clone3				
AR049	Corn Clone4	Corn Clone4			T	
AR050	Donor II B Cells 24hrs	Donor II B Cells				
AR051	Donor II B Cells 72hrs	24hrs Donor II B Cells	-		<del>                                     </del>	
		72hrs			<del> </del>	
AR052	Donor II B-Cells 24 hrs.	Donor II B-Cells 24 hrs.				
AR053	Donor II B-Cells 72hrs	Donor II B-Cells 72hrs				
AR054	Donor II Resting B Cells	Donor II Resting B Cells				
AR055	Heart	Heart	<del> </del>		1	T
AR056	Human Lung (clonetech)	Human Lung (clonetech)				
AR057	Human Mammary	Human Manunary			,	
AR058	(clontech) Human Thymus	(clontech) Human Thymus			1	
AR059	(clonetech)  Jurkat (unstimulated)	(clonetech)  Jurkat	<del> </del>		<del> </del>	<del>                                     </del>
	· ·	(unstimulated) Kidney			<del> </del>	
AR060	Kidney		+		+	
AR061	Liver	Liver (Clartech)			+	
AR062	Liver (Clontech)	Liver (Clontech)				<del></del>
AR063	Lymphocytes chronic	Lymphocytes	<u> .l </u>			

	lymphocytic leukaemia	chronic lymphocytic			<u> </u>	
		leukaemia				
AR064	Lymphocytes diffuse large	Lymphocytes diffuse large B cell	ļ			}
	B cell lymphoma	lymphoma				
AR065	Lymphocytes follicular	Lymphocytes				
	lymphoma	follicular lymphoma			ļ	ļ
AR066	normal breast	normal breast				
AR067	Normal Ovarian (4004901)	Normal Ovarian (4004901)				
AR068	Normal Ovary 9508G045	Normal Ovary 9508G045				
AR069	Normal Ovary 9701G208	Normal Ovary 9701G208				
AR070	Normal Ovary 9806G005	Normal Ovary 9806G005				
AR071	Ovarian Cancer	Ovarian Cancer			ļ	
AR072	Ovarian Cancer (9702G001)	Ovarian Cancer (9702G001)				
AR073	Ovarian Cancer	Ovarian Cancer				
14075	(9707G029)	(9707G029)			<u> </u>	<u> </u>
AR074	Ovarian Cancer	Ovarian Cancer		ļ.		
AR075	(9804G011) Ovarian Cancer	(9804G011) Ovarian Cancer				<del> </del>
144073	(9806G019)	(9806G019)			<u> </u>	
AR076	Ovarian Cancer	Ovarian Cancer			]	}
AR077	(9807G017) Ovarian Cancer	(9807G017) Ovarjan Cancer			<del> </del>	<del> </del>
AROTT	(9809G001)	(9809G001)			<u> </u>	
AR078	ovarian cancer 15799	ovarian cancer 15799				
AR079	Ovarian Cancer 17717AID	Ovarian Cancer 17717AID				
AR080	Ovarian Cancer 4004664B1	Ovarian Cancer 4004664B1		,		
AR081	Ovarian Cancer 4005315A1	Ovarian Cancer 4005315A1				
AR082	ovarian cancer 94127303	ovarian cancer				
		94127303	ļ		<u> </u>	
AR083	Ovarian Cancer 96069304	Ovarian Cancer 96069304			<u> </u>	
AR084	Ovarian Cancer 9707G029	Ovarian Cancer 9707G029				
AR085	Ovarian Cancer 9807G045	Ovarian Cancer 9807G045				<u> </u>
AR086	ovarian cancer 9809G001	ovarian cancer 9809G001				
AR087	Ovarian Cancer 9905C032RC	Ovarian Cancer 9905C032RC				
AR088	Ovarian cancer 9907 C00 3rd	Ovarian cancer 9907 C00 3rd				
AR089	Prostate	Prostate	<del> </del>		<u></u>	
AR090	Prostate (clonetech)	Prostate (clonetech) prostate cancer	<del> </del>		+	<del></del>
AR091 AR092	prostate cancer #15176	prostate cancer	<del> </del> -	<del>                                     </del>	<del> </del>	1
		#15176		ļ		<del></del>
AR093	prostate cancer #15509	prostate cancer #15509				
AR094	prostate cancer #15673	prostate cancer #15673				
AR095	Small Intestine (Clontech)	Small Intestine (Clontech)				

AR096	Spleen	Spleen			
AR097	Thymus T cells activated	Thymus T cells			
	,	activated	i		
AR098	Thymus T cells resting	Thymus T cells			
		resting			
AR099	Tonsil	Tonsil			
AR100	Tonsil geminal center	Tonsil geminal	i		
	centroblast	center centroblast			
AR101	Tonsil germinal center B	Tonsil germinal			
	cell	center B cell			
AR102	Tonsil lymph node	Tonsil lymph node	· <del>,</del>		
AR103	Tonsil memory B cell	Tonsil memory B cell			
10101	Miles I. Design	Whole Brain			
AR104	Whole Brain	Xenograft ES-2		<del></del>	<del></del>
AR105	Xenograft ES-2	Xenograft SW626			<del></del>
AR106 H0002	Xenograft SW626 Human Adult Heart	Human Adult Heart	Heart		Uni-ZAP XR
H0002	Human Adult Liver	Human Adult Liver	Liver		Uni-ZAP XR
H0003	Human Adult Spleen	Human Adult	Spleen		Uni-ZAP XR
110004	Human Adun Spicen	Spleen	Брисси	1	
H0008	Whole 6 Week Old	- Opioon			Uni-ZAP XR
1.10000	Embryo				
H0009	Human Fetal Brain				Uni-ZAP XR
H0011	Human Fetal Kidney	Human Fetal Kidney	Kidney		Uni-ZAP XR
H0012	Human Fetal Kidney	Human Fetal Kidney	Kidney		Uni-ZAP XR
H0013	Human 8 Week Whole	Human 8 Week Old	Embryo		Uni-ZAP XR
	Embryo	Embryo			
H0014	Human Gall Bladder	Human Gall Bladder	Gall Bladder		Uni-ZAP XR
H0015 ·	Human Gall Bladder,	Human Gall Bladder	Gall Bladder		Uni-ZAP XR
	fraction II				
H0018	Human Greater Omentum,	Human Greater	peritoneum		Uni-ZAP XR
	fII remake	Omentum			-Dlucarint
H0019	Human Fetal Heart	Human Fetal Heart	Heart	<del> </del>	pBluescript Uni-ZAP XR
H0020	Human Hippocampus	Human	Brain		UIII-ZAF AK
770000	Jurkat Cells	Hippocampus  Jurkat T-Cell Line		<del> </del>	Lambda
H0022	Jurkat Cells	Jurkat 1-Cell Line			ZAP II
H0023 ·	Human Fetal Lung		<del> </del>		Uni-ZAP XR
H0023	Human Fetal Lung III	Human Fetal Lung	Lung		Uni-ZAP XR
H0026	Namalwa Cells	Namalwa B-Cell			Lambda
110020	I Tallial Wa Colls	Line, EBV			ZAP II
		immortalized		( (	
H0027	Human Ovarian Cancer			disease	Uni-ZAP XR
H0028	Human Old Ovary	Human Old Ovary	Ovary		pBluescript
H0030	Human Placenta				Uni-ZAP XR
H0031	Human Placenta	Human Placenta	Placenta		Uni-ZAP XR
H0032	Human Prostate	Human Prostate	Prostate		Uni-ZAP XR
H0033	Human Pituitary	Human Pituitary			Uni-ZAP XR
H0035	Human Salivary Gland	Human Salivary	Salivary		Uni-ZAP XR
		Gland	gland		
H0036	Human Adult Small	Human Adult Small	Small Int.		Uni-ZAP XR
	Intestine	Intestine	<del> </del>		-Diversit
H0037	Human Adult Small	Human Adult Small	Small Int.		pBluescript
	Intestine	Intestine	- m		Hei ZAB VB
H0038	Human Testes	Human Testes	Testis	3!	Uni-ZAP XR Uni-ZAP XR
H0039	Human Pancreas Tumor	Human Pancreas	Pancreas	disease	Uni-ZAP XR
	1	Tumor	TD: -1:-	disease	Uni-ZAP XR
H0040	Human Testes Tumor	Human Testes	Testis	disease	OIU-ZAF AR
H0041	Human Fetal Bone	Tumor Human Fetal Bone	Bone	<del> </del>	Uni-ZAP XR
	i muman reial Bone	L CONTRACTERAL MODE	שווטכו	1 1	J J / LIC
H0041	Human Adult Pulmonary	Human Adult	Lung		Uni-ZAP XR

H0046	Human Endometrial	Human Endometrial	Uterus		disease	Uni-ZAP XR
	Tumor	Tumor	Liver			Uni-ZAP XR
H0047	Human Fetal Liver	Human Fetal Liver	Kidney			Uni-ZAP XR
H0049	Human Fetal Kidney	Human Fetal Kidney	Heart			Uni-ZAP XR
H0050	Human Fetal Heart	Human Fetal Heart	Brain			Uni-ZAP XR
H0051	Human Hippocampus	Human Hippocampus	aiste			
H0052	Human Cerebellum	Human Cerebellum	Brain			Uni-ZAP XR
H0056	Human Umbilical Vein,	Human Umbilical	Umbilical			Uni-ZAP XR
110030	Endo. remake	Vein Endothelial Cells	vein			
H0057	Human Fetal Spleen					Uni-ZAP XR
H0058	Human Thymus Tumor	Human Thymus Tumor	Thymus		disease	Lambda ZAP II
H0059	Human Uterine Cancer	Human Uterine	Uterus		disease	Lambda ZAP II
		Cancer				pBluescript
H0060	Human Macrophage	Human Macrophage	Blood	Cell Line		
H0061	Human Macrophage	Human Macrophage	Blood	Cell Line		pBluescript
H0063	Human Thymus	Human Thymus	Thymus_	<b> </b>		Uni-ZAP XR
H0068	Human Skin Turnor	Human Skin Tumor	Skin		disease	Uni-ZAP XR
H0069	Human Activated T-Cells	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0070	Human Pancreas	Human Pancreas	Pancreas	<u> </u>		Uni-ZAP XR
H0071	Human Infant Adrenal	Human Infant	Adrenal	1		Uni-ZAP XR
110071	Gland	Adrenal Gland	gland	<u> </u>		
H0079	Human Whole 7 Week	Human Whole 7	Embryo	1		Uni-ZAP XR
110475	Old Embryo (II)	Week Old Embryo				
H0080	Human Whole 6 Week	Human Whole Six	Embryo	1		Lambda
110000	Old Embryo (II)	Week Old Embryo	·	1		ZAPII
H0081	Human Fetal Epithelium (Skin)	Human Fetal Skin	Skin	,		Uni-ZAP XR
H0083	HUMAN JURKAT MEMBRANE BOUND POLYSOMES	Jurkat Cells				Uni-ZAP XR
H0085	Human Colon	Human Colon				Lambda ZAP II
H0086	Human epithelioid	Epithelioid	Sk Muscle		disease	Uni-ZAP XR
	sarcoma	Sarcoma, muscle		ļ		pBluescript
H0087	Human Thymus	Human Thymus			12	Uni-ZAP XR
H0090	Human T-Cell Lymphoma	T-Cell Lymphoma	T-Cell		disease	Lambda
H0096	Human Parotid Cancer	Human Parotid Cancer	Parotid		disease	ZAP II
H0097	Human Adult Heart, subtracted	Human Adult Heart	Heart			pBluescript
H0098	Human Adult Liver, subtracted	Human Adult Liver	Liver			Uni-ZAP XR
H0099	Human Lung Cancer, subtracted	Human Lung Cancer	Lung			pBluescript
H0100	Human Whole Six Week Old Embryo	Human Whole Six Week Old Embryo	Embryo			Uni-ZAP XF
H0101	Human 7 Weeks Old Embryo, subtracted	Human Whole 7 Week Old Embryo	Embryo			Lambda ZAP II
H0102		Human Whole Six Week Old Embryo	Embryo			pBluescript
H0105		Human Fetal Heart	Heart			pBluescript
H0107		Human Infant Adrenal Gland	Adrenal gland			pBluescript
H0109		Macrophage	Blood	Cell Line		pBluescript
H0111		Human Placenta	Placenta			pBluescript
	Human Thymus Tumor,	Human Thymus	Thymus	F		pBluescript_

		Tumor				
H0119	subtracted Human Pediatric Kidney	Human Pediatric	Kidney			Uni-ZAP XR
HULLY	Human rediante Kluney	Kidney		1		
H0121	Human Cornea, subtracted	Human Cornea	eye			Uni-ZAP XR
H0122	Human Adult Skeletal	Human Skeletal	Sk Muscle			Uni-ZAP XR
110122	Muscle	Muscle				
H0123	Human Fetal Dura Mater	Human Fetal Dura	Brain			Uni-ZAP XR
110.23		Mater		L		
H0124	Human	Human	Sk Muscle	1	disease	Uni-ZAP XR
	Rhabdomyosarcoma	Rhabdomyosarcoma				V : (7 t D V D
H0125	Cem cells cyclohexamide	Cyclohexamide	Blood	Cell Line	'	Uni-ZAP XR
	treated	Treated Cem, Jurkat,		1		
_		Raji, and Supt				Uni-ZAP XR
H0129	Jurkat cells, thiouridine	Jurkat Cells				Uni-ZAF AK
	activated, fract II			G II I in a		Uni-ZAP XR
H0130	LNCAP untreated	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
H0131	LNCAP + 0.3nM R1881	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
H0132	LNCAP + 30nM R1881	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
H0134	Raji Cells, cyclohexamide	Cyclohexamide	Blood	Cell Line		UIII-ZAI AK
	treated	Treated Cem, Jurkat,		1 1		
		Raji, and Supt		<del> </del>		Uni-ZAP XR
H0135	Human Synovial Sarcoma	Human Synovial	Synovium	[ ]		OM-ZAL ALK
		Sarcoma	Disad	Cell Line		Uni-ZAP XR
H0136	Supt Cells, cyclohexamide	Cyclohexamide	, Blood	Cell Line		l om-za a xxx
	treated	Treated Cem, Jurkat,				į ·
		Raji, and Supt	Blood	Cell Line		Uni-ZAP XR
H0140	Activated T-Cells, 8 hrs.	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0141	Activated T-Cells, 12 hrs.	Activated T-Cells		Cen Line		Uni-ZAP XR
H0144	Nine Week Old Early	9 Wk Old Early	Embryo			Oili-Eili iii
	Stage Human	Stage Human Human Whole 7	Embryo	<del> </del>		Uni-ZAP XR
H0149	7 Week Old Early Stage		Embryo			
	Human, subtracted	Week Old Embryo	Testis	<del></del>		Uni-ZAP XR
H0150	Human Epididymus	Epididymis Human Skin	Skin	<del>- </del> -i	disease	Uni-ZAP XR
H0154	Human Fibrosarcoma	Fibrosarcoma	Skiii		0.00.00	
		Human Adrenal	Adrenal		disease	Uni-ZAP XR
H0156	Human Adrenal Gland	Gland Tumor	Gland	1	0.00000	
	Tumor	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0159	Activated T-Cells, 8 hrs.,	Activated 1-Cens	Blood	) Con Zime		
110161	ligation 2 Activated T-Cells, 24 hrs.,	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0161	ligation 2	Activated 1-cens	2.000		}	
H0163	Human Synovium	Human Synovium	Synovium			Uni-ZAP XR
H0164		Human Trachea	Trachea		disease	Uni-ZAP XR
H0104	Human Trachea Tumor	Tumor		ļ	<u></u>	
H0165	Human Prostate Cancer,	Human Prostate	Prostate		disease	Uni-ZAP XR
110103	Stage B2	Cancer, stage B2	ł			
H0166	Human Prostate Cancer,	Human Prostate	Prostate		disease	Uni-ZAP XR
110100	Stage B2 fraction	Cancer, stage B2	1	· ·		
H0168		Human Prostate	Prostate		disease	Uni-ZAP XR
110103	Stage C	Cancer, stage C	1		·	
H0169	Human Prostate Cancer,	Human Prostate	Prostate		disease	Uni-ZAP XR
110105	Stage C fraction	Cancer, stage C			<u> </u>	
H0170		Twelve Week Old	Embryo			Uni-ZAP XR
	Human	Early Stage Human				<del> </del>
H0171		Twelve Week Old	Embryo		1	Uni-ZAP XR
	Human, II	Early Stage Human	<u> </u>			<del></del>
H0172		Human Fetal Brain	Brain			Lambda
	random primed				<u> </u>	ZAP II
H0173		Human	Heart	1	disease	Uni-ZAP XR
	RNA remake	Cardiomyopathy			<del> </del>	-C1
H0175	H. Adult Spleen, ziplox				<del></del>	pSport1 Uni-ZAP XR
H0177		CAMA1 Ee Cell	Breast	Cell Line		Uni-ZAP XR

		Line				II : ZADVD
110178	Human Fetal Brain	Human Fetal Brain	Brain			Uni-ZAP XR
H0179	Human Neutrophil	Human Neutrophil	Blood	Cell Line		Uni-ZAP XR
H0181	Human Primary Breast Cancer	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0182	Human Primary Breast Cancer	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0184	Human Colon Cancer, metasticized to live	Human Colon Cancer, metasticized to liver	Liver		disease	Lambda ZAP II
H0186	Activated T-Cell	T-Cells	Blood	Cell Line		Lambda ZAP II
H0187	Resting T-Cell	T-Cells	Blood	Cell Line		Lambda ZAP II
H0188	Human Normal Breast	Human Normal Breast	Breast		. <u> </u>	Uni-ZAP XR
H0189	Human Resting Macrophage	Human Macrophage/Monoc ytes	Blood	Cell Line		Uni-ZAP XR
H0190	Human Activated Macrophage (LPS)	Human Macrophage/Monoc ytes	Blood	Cell Line		Uni-ZAP XR
H0191	Human Activated Macrophage (LPS), thiour	Human Macrophage/Monoc ytes	Blood	Cell Line		Uni-ZAP XR
H0192	Cem Cells, cyclohexamide treated, subtra	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		Uni-ZAP XR
H0194	Human Cerebellum,	Human Cerebellum	Brain			pBluescript
H0196	Human Cardiomyopathy, subtracted	Human Cardiomyopathy	Heart			Uni-ZAP XR
H0197	Human Fetal Liver, subtracted	Human Fetal Liver	Liver			Uni-ZAP XR
H0199	Human Fetal Liver, subtracted, neg clone	Human Fetal Liver	Liver			Uni-ZAP XR
H0200	Human Greater Omentum, fract II remake,	Human Greater Omentum	peritoneum			Uni-ZAP XR
H0201	Human Hippocampus, subtracted	Human Hippocampus	Brain			pBluescript
H0204	Human Colon Cancer, subtracted	Human Colon Cancer	Colon			pBluescript
H0207	LNCAP, differential expression	LNCAP Cell Line	Prostate	Cell Line		pBluescript
H0208	Early Stage Human Lung, subtracted	Human Fetal Lung	Lung			pBluescript
H0212	Human Prostate, subtracted	Human Prostate	Prostate			pBluescript
H0213	Human Pituitary, subtracted	Human Pituitary				Uni-ZAP XR
H0214	Raji cells, cyclohexamide treated, subtracted	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		pBluescript
H0216	Supt cells, cyclohexamide treated, subtracted	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		pBluescript
H0220	Activated T-Cells, 4 hrs, subtracted	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0221	Activated T-Cells, 4 hrs, differentially expressed	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0224	Activated T-Cells, 12 hrs, subtracted	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0229	Early Stage Human Brain,	Early Stage Human	Brain		<u> </u>	Lambda

	random primed	Brain				ZAPII
H0230	Human Cardiomyopathy,	Human	Heart		disease	Uni-ZAP XR
	diff exp	Cardiomyopathy				
H0231	Human Colon, subtraction	Human Colon				pBluescript
H0232	Human Colon, differential expression	Human Colon				pBluescript
H0234	human colon cancer, metastatic to liver, differentially expressed	Human Colon Cancer, metasticized to liver	Liver		_	pBluescript
H0239	Human Kidney Tumor	Human Kidney Tumor	Kidney		disease	Uni-ZAP XR
H0240	C7MCF7 cell line, estrogen treated, Differential	C7MCF7 Cell Line, estrogen treated	Breast	Cell Line		Uni-ZAP XR
H0241	C7MCF7 cell line, estrogen treated, subtraction	C7MCF7 Cell Line, estrogen treated	Breast	Cell Line		Uni-ZAP XR
H0242	Human Fetal Heart, Differential (Fetal- Specific)	Human Fetal Heart	Heart			pBluescript
H0244	Human 8 Week Whole Embryo, subtracted	Human 8 Week Old Embryo	Embryo			Uni-ZAP XR
H0245	Human 8 Week Whole Embryo, differential	Human 8 Weck Old Embryo	Embryo			Uni-ZAP XR
H0246	Human Fetal Liver- Enzyme subtraction	Human Fetal Liver	Liver			Uni-ZAP XR
H0247	Human Membrane Bound Polysomes- Enzyme Subtraction	Human Membrane Bound Polysomes	Blood	Cell Line		Uni-ZAP XR
H0249	HE7, subtracted by hybridization with E7 cDNA	Human Whole 7 Week Old Embryo	Embryo			Uni-ZAP XR
H0250	Human Activated Monocytes	Human Monocytes				Uni-ZAP XR
H0251	Human Chondrosarcoma	Human Chondrosarcoma	Cartilage		disease	Uni-ZAP XR
H0252	Human Osteosarcoma	Human Osteosarcoma	Bone		disease	Uni-ZAP XR
H0253	Human adult testis, large inserts	Human Adult Testis	Testis			Uni-ZAP XR
H0254	Breast Lymph node cDNA library	Breast Lymph Node	Lymph Node			Uni-ZAP XR
H0255	breast lymph node CDNA library	Breast Lymph Node	Lymph Node			Lambda ZAP II
H0256	HL-60, unstimulated	Human HL-60 Cells, unstimulated	Blood	Cell Line		Uni-ZAP XR
H0257	HL-60, PMA 4H	HL-60 Cells, PMA stimulated 4H	Blood	Cell Line		Uni-ZAP XR
H0261	H. cerebellum, Enzyme subtracted	Human Cerebellum	Brain			Uni-ZAP XR
H0263	human colon cancer	Human Colon Cancer	Colon		disease	Lambda ZAP II
H0264	human tonsils	Human Tonsil	Tonsil			Uni-ZAP XR
H0265	Activated T-Cell (12hs)/Thiouridine labelledEco	T-Cells	Blood	Cell Line		Uni-ZAP XR
H0266	Human Microvascular Endothelial Cells, fract. A	HMEC	Vein	Cell Line		Lambda ZAP II
H0267	Human Microvascular Endothelial Cells, fract. B	HMEC	Vein	Cell Line		Lambda ZAP II
H0268	Human Umbilical Vein Endothelial Cells, fract. A	HUVE Cells	Umbilical vein	Cell Line		Lambda ZAP II
H0269	Human Umbilical Vein	HUVE Cells	Umbilical	Cell Line	<u>L</u>	Lambda

<del></del> -1	Endothelial Cells, fract. B	·····	vein			ZAP II
H0270	HPAS (human pancreas, subtracted)	Human Pancreas	Pancreas			Uni-ZAP XR
H0271	Human Neutrophil, Activated	Human Neutrophil - Activated	Blood	Cell Line		Uni-ZAP XR
H0272	HUMAN TONSILS, FRACTION 2	Human Tonsil	Tonsil			Uni-ZAP XR
H0274	Human Adult Spleen, fraction II	Human Adult Spieen	Spleen			Uni-ZAP XR
H0275	Human Infant Adrenal Gland, Subtracted	Human Infant Adrenal Gland	Adrenal gland			pBluescript
H0280	K562 + PMA (36 hrs)	K562 Cell line	cell line	Cell Line		ZAP Express
H0282	HBGB"s differential	Human Primary Breast Cancer	Breast			Uni-ZAP XR
H0284	Human OB MG63 control fraction I	Human Osteoblastoma MG63 cell line	Bone	Cell Line		Uni-ZAP XR
H0286	Human OB MG63 treated (10 nM E2) fraction I	Human Osteoblastoma MG63 cell line	Bone	Cell Line		Uni-ZAP XR
H0288	Human OB HOS control fraction I	Human Osteoblastoma HOS cell line	Bone	Cell Line		Uni-ZAP XR
H0290	Human OB HOS treated (1 nM E2) fraction I	Human Osteoblastoma HOS cell line	Bone	Cell Line		Uni-ZAP XR
H0292	Human OB HOS treated (10 nM E2) fraction I	Human Osteoblastoma HOS cell line	Bone	Cell Line		Uni-ZAP XR
H0293	WI 38 cells					Uni-ZAP XR
H0294	Amniotic Cells - TNF induced	Amniotic Cells - TNF induced	Placenta	Cell Line		Uni-ZAP XR
H0295	Amniotic Cells - Primary Culture	Amniotic Cells - Primary Culture	Placenta	Cell Line		Uni-ZAP XR
H0305	CD34 positive cells (Cord Blood)	CD34 Positive Cells	Cord Blood			ZAP Express
· H0306	CD34 depleted Buffy Coat (Cord Blood)	CD34 Depleted Buffy Coat (Cord Blood)	Cord Blood			ZAP Express
H0309	Human Chronic Synovitis	Synovium, Chronic Synovitis/ Osteoarthritis	Synovium		disease	Uni-ZAP XR
H0310	human caudate nucleus	Brain	Brain			Uni-ZAP XR
H0316	HUMAN STOMACH	Human Stomach	Stomach			Uni-ZAP XR
H0318	HUMAN B CELL LYMPHOMA	Human B Cell Lymphoma	Lymph Node		disease	Uni-ZAP XR
H0321	HUMAN SCHWANOMA	Schwanoma	Nerve	<u> </u>	disease	Uni-ZAP XR
H0327	human corpus colosum	Human Corpus Callosum	Brain			Uni-ZAP XR
H0328	human ovarian cancer	Ovarian Cancer	Ovary	<b> </b>	disease	Uni-ZAP XR
H0329	Dermatofibrosarcoma Protuberance	Dermatofibrosarcom a Protuberans	Skin		disease	Uni-ZAP XR
H0331	Hepatocellular Tumor	Hepatocellular Tumor	Liver		disease	Lambda ZAP II
H0333	Hemangiopericytoma	Hemangiopericytom a	Blood vessel		disease	Lambda ZAP II
H0334	Kidney cancer	Kidney Cancer	Kidney	<u> </u>	disease	Uni-ZAP XR
H0339		Duodenum				Uni-ZAP XR
H0340	Corpus Callosum	Corpus Collosum- 93052				Uni-ZAP XR
H0341	Bone Marrow Cell Line (RS4;11)	Bone Marrow Cell Line RS4;11	Bone Marrow	Cell Line		Uni-ZAP XR

					diagona	Uni-ZAP XR
H0343	stomach cancer (human)	Stomach Cancer - 5383A (human)			disease	
H0344	Adipose tissue (human)	Adipose - 6825A (human)				Uni-ZAP XR
770246	Brain-medulloblastoma	Brain	Brain		disease	Uni-ZAP XR
H0346	Brain-medulionasionia	(Medulloblastoma)- 9405C006R	Diam			
H0349	human adult liver cDNA library	Human Adult Liver	Liver			pCMVSport 1
H0351	Glioblastoma	Glioblastoma	Brain		disease	Uni-ZAP XR
H0352	wilm's tumor	Wilm"s Tumor			disease	Uni-ZAP XR
H0354	Human Leukocytes	Human Leukocytes	Blood	Cell Line		pCMVSport
H0355	Human Liver	Human Liver, normal Adult				pCMVSport
H0356	Human Kidney	Human Kidney	Kidney			pCMVSport
H0357	H. Normalized Fetal Liver, II	Human Fetal Liver	Liver			Uni-ZAP XR
110250	KMH2 cell line	КМН2				ZAP Express
H0359 H0361	Human rejected kidney	Human Rejected Kidney			disease	pBluescript
H0364	Human Osteoclastoma,	Human Osteoclastoma			disease	pBluescript
H0365	Osteoclastoma-normalized	Human Osteoclastoma			disease	Uni-ZAP XR
110266	B L428 cell line	L428				ZAP Express
H0366	H. Atrophic Endometrium	Atrophic		<del> </del>		Uni-ZAP XR
H0369	H. Atrophic Endometrium	Endometrium and myometrium				
H0370	H. Lymph node breast Cancer	Lymph node with Met. Breast Cancer			disease	Uni-ZAP XR
H0373	Human Heart	Human Adult Heart	Heart			pCMVSport
H0374	Human Brain	Human Brain				pCMVSport 1
H0375	Human Lung	Human Lung				pCMVSport 1
H0376	Human Spleen	Human Adult Spleen	Spleen			pCMVSport 1
H0379	Human Tongue, frac 1	Human Tongue				pSport1
H0380	Human Tongue, frac 2	Human Tongue				pSport1
H0381	Bone Cancer	Bone Cancer			disease	Uni-ZAP XI
H0383	Human Prostate BPH, re-	Human Prostate BPH				Uni-ZAP XI
H0388	Human Rejected Kidney, 704 re-excision	Human Rejected Kidney			disease	pBluescript
H0390	Human Amygdala Depression, re-excision	Human Amygdala Depression			disease	pBluescript
H0391	H. Meniingima, M6	Human Meningima	brain			pSport1
H0392	H. Meningima, M1	Human Meningima	brain			pSport1
H0393	Fetal Liver, subtraction II	Human Fetal Liver	Liver			pBluescript
H0394	A-14 cell line	Redd-Stemberg cell				ZAP Expres
H0395	A1-CELL LINE	Redd-Sternberg cell				ZAP Expres
H0396		Redd-Sternberg cell				ZAP Expres
H0399		Human Kidney Cortex				Lambda ZAP II
H0400		Human Brain, Striatum Depression	Brain			Lambda ZAP II
H0401	Human Pituitary,	Human Pituitary				pBluescript
1	subtracted V	1				ZAP Expres

	(Cord Blood), re-excision	Buffy Coat (Cord	<del></del>	T		T
		Blood)				
H0403	H. Umbilical Vein Endothelial Cells, IL4 induced	HUVE Cells	Umbilical vein	Cell Line		Uni-ZAP XR
H0404	-H. Umbilical Vein endothelial cells, uninduced	HUVE Cells	Umbilical vein	Cell Line		Uni-ZAP XR
H0408	Human kidney Cortex, subtracted	Human Kidney Cortex				pBluescript
H0409	H. Striatum Depression, subtracted	Human Brain, Striatum Depression	Brain			pBluescript
H0411	H Female Bladder, Adult	Human Female Adult Bladder	Bladder			pSport1
H0412	Human umbilical vein endothelial cells, IL-4 induced	HUVE Cells	Umbilical vein	Cell Line		pSport1
H0413	Human Umbilical Vein Endothelial Cells, uninduced	HUVE Cells	Umbilical vein	Cell Line		pSport1
H0415	H. Ovarian Tumor, II, OV5232	Ovarian Tumor, OV5232	Ovary		disease	pCMVSport 2.0
H0416	Human Neutrophils, Activated, re-excision	Human Neutrophil - Activated	Blood	Cell Line		pBluescript
H0417	Human Pituitary, subtracted VIII	Human Pituitary				pBluescript
H0419	Bone Cancer, re-excision	Bone Cancer		<u> </u>		Uni-ZAP XR
H0421	Human Bone Marrow, re- excision	Bone Marrow				pBluescript
H0422	T-Cell PHA 16 hrs	T-Cells	Blood	Cell Line		pSport1
H0423	T-Cell PHA 24 hrs	T-Cells	Blood	Cell Line		pSport1
H0424	Human Pituitary, subt IX	Human Pituitary				pBluescript
H0427	Human Adipose	Human Adipose, left hiplipoma				pSport1
H0428	Human Ovary	Human Ovary Tumor	Ovary			pSport1
H0429	K562 + PMA (36 hrs),re- excision	K562 Cell line	cell line	Cell Line		ZAP Express
H0431	H. Kidney Medulla, re- excision	Kidney medulla	Kidney		· · · · · · · · · · · · · · · · · · ·	pBluescript
H0433	Human Umbilical Vein Endothelial cells, frac B, re-excision	HUVE Cells	Umbilical vein	Cell Line		pBluescript
H0434	Human Brain, striatum, re-excision	Human Brain, Striatum				pBluescript
H0435	Ovarian Turnor 10-3-95	Ovarian Tumor, OV350721	Ovary			pCMVSport 2.0
H0436	Resting T-Cell Library,II	T-Cells	Blood	Cell Line		pSport1
H0437	H Umbilical Vein Endothelial Cells, frac A, re-excision	HUVE Cells	Umbilical vein	Cell Line		Lambda ZAP II
H0438	H. Whole Brain #2, re- excision	Human Whole Brain #2				ZAP Express
H0440	FGF enriched mixed library	Mixed libraries				pCMVSport
H0441	H. Kidney Cortex, subtracted	Kidney cortex	Kidney			pBluescript
H0443	H. Adipose, subtracted	Human Adipose, left hiplipoma	•			pSport1
H0444	Spleen metastic melanoma	Spleen, Metastic malignant melanoma	Spleen		disease	pSport1
H0445	Spleen, Chronic	Human Spleen, CLL	Spleen	J	disease	pSport1

	lymphocytic leukemia				<del></del>	
H0448	Salivary gland, subtracted	Human Salivary	Salivary			Lambda
770440	CD24: II I	Gland	gland	<del>                                     </del>		ZAP II pSport1
H0449	CD34+ cell, I	CD34 positive cells	TC: do acc	<u> </u>		pBluescript
H0453	H. Kidney Pyramid, subtracted	Kidney pyramids	Kidney			<u> </u>
H0455	H. Striatum Depression, subt	Human Brain, Striatum Depression	Brain			pBluescript
H0456	H Kidney Cortex, subtracted III	Human Kidney Cortex				pBluescript .
H0457	Human Eosinophils	Human Eosinophils				pSport1
H0458	CD34+ cell, I, frac II	CD34 positive cells				pSport1
H0459	CD34+cells, II, FRACTION 2	CD34 positive cells				pCMVSport 2.0
H0477	Human Tonsil, Lib 3	Human Tonsil	Tonsil			pSport1
H0478	Salivary Gland, Lib 2	Human Salivary Gland	Salivary gland			pSport1
H0479	Salivary Gland, Lib 3	Human Salivary Gland	Salivary gland			pSport1
H0483	Breast Cancer cell line, MDA 36	Breast Cancer Cell line, MDA 36				pSport1
H0484	Breast Cancer Cell line,	Breast Cancer Cell				pSport1
	angiogenic	line, Angiogenic, 36T3				
H0485	Hodgkin"s Lymphoma I	Hodgkin"s Lymphoma I			disease	pCMVSport 2.0
H0486	Hodgkin"s Lymphoma II	Hodgkin"s Lymphoma II	-		disease	pCMVSport 2.0
H0487	Human Tonsils, lib I	Human Tonsils				pCMVSport 2.0
H0488	Human Tonsils, Lib 2	Human Tonsils				pCMVSport 2.0
H0489	Crohn"s Disease	Ileum	Intestine		disease	pSport1
H0492	HL-60, RA 4h, Subtracted	HL-60 Cells, RA stimulated for 4H	Blood	Cell Line		Uni-ZAP XF
H0494	Keratinocyte	Keratinocyte			i	pCMVSport 2.0
H0497	HEL cell line	HEL cell line		HEL 92.1.7		pSport1
H0505	Human Astrocyte	Human Astrocyte				pSport1
H0506	Ulcerative Colitis	Colon	Colon			pSport1
H0509	Liver, Hepatoma	Human-Liver, Hepatoma, patient 8	Liver		disease	pCMVSport 3.0
H0510	Human Liver, normal	Human Liver, normal, Patient # 8	Liver			pCMVSport
H0512	Keratinocyte, lib 3	Keratinocyte				pCMVSport 2.0
H0517	Nasal polyps	Nasal polyps				pCMVSport
H0518	pBMC stimulated w/ poly	pBMC stimulated with poly I/C				pCMVSport
H0519	NTERA2, control	NTERA2, Teratocarcinoma cell line				pCMVSport
H0520	NTERA2 + retinoic acid, 14 days	NTERA2, Teratocarcinoma cell line				pSport1
H0521	Primary Dendritic Cells, lib 1	Primary Dendritic cells				pCMVSport 3.0
H0522	Primary Dendritic cells, frac 2	Primary Dendritic cells				pCMVSport 3.0
H0525	PCR, pBMC I/C treated	pBMC stimulated				PCRII

		with poly I/C			<del></del>	1
H0528	Poly[I]/Poly[C] Normal	Poly[I]/Poly[C]				pCMVSport
j	Lung Fibroblasts	Normal Lung				3.0
		Fibroblasts				
H0529	Myoloid Progenitor Cell	TF-1 Cell Line;		i .		pCMVSport
İ	Line	Myoloid progenitor				3.0
***		cell line		L		
H0530	Human Dennal	Human Dermal				pSport1
	Endothelial	Endothelial Cells;				1
H0535	Cells,untreated  Human ovary tumor cell	untreated Ovarian Tumor,	Ovary		disease	pSport1
LOSSS	OV350721	OV350721	Ovary		discase	paporti
H0537	H. Primary Dendritic	Primary Dendritic				pCMVSport
110557	Cells, lib 3	cells				2.0
H0538	Merkel Cells	Merkel cells	Lymph node		<del></del>	pSport1
H0539	Pancreas Islet Cell Tumor	Pancreas Islet Cell	Pancreas		disease	pSport1
110337	Tunoredo Islat Com Tunior	Tumour	7 411-1-0110			1-1-
H0540	Skin, burned	Skin, leg burned	Skin			pSport1
H0542	T Cell helper I	Helper T cell				pCMVSport
	•	·				3.0
H0543	T cell helper II	Helper T cell				pCMVSport
						3.0
H0544	Human endometrial	Human endometrial	l			pCMVSport
	stromal cells	stromal cells				3.0
H0545	Human endometrial	Human endometrial				pCMVSport
	stromal cells-treated with	stromal cells-treated	}			3.0
	progesterone	with proge				- C) (1/C
H0546	Human endometrial	Human endometrial stromal cells-treated		1		pCMVSport 3.0
	stromal cells-treated with estradiol	with estra		i		3.0
H0547	NTERA2 teratocarcinoma	NTERA2.				pSport1
110347	cell line+retinoic acid (14	Teratocarcinoma	1			poporti
	days)	cell line	]			
H0549	H. Epididiymus, caput &	Human	<del></del>			Uni-ZAP XR
	corpus	Epididiymus, caput		l i		
	1	and corpus				1
H0550	H. Epididiymus, cauda	Human				Uni-ZAP XR
		Epididiymus, cauda				<u> </u>
H0551	Human Thymus Stromal	Human Thymus				pCMVSport
*****	Cells	Stromal Cells				3.0
H0553	Human Placenta	Human Placenta	İ			pCMVSport 3.0
H0555	Rejected Kidney, lib 4	Human Rejected	Kidney		disease	pCMVSport
HUSSS	Rejected Kidney, no 4	Kidney	Kidney		Uiscase	3.0
H0556	Activated T-	T-Cells	Blood	Cell Line		Uni-ZAP XR
110550	cell(12h)/Thiouridine-re-	1-cens	Diood	Con Dine		0111 2111
	excision					ļ
H0559	HL-60, PMA 4H, re-	HL-60 Cells, PMA	Blood	Cell Line		Uni-ZAP XR
	excision	stimulated 4H				
H0560	КМН2	KMH2				pCMVSport
	, .,,	1	<u> </u>			3.0
H0561	L428	L428				pCMVSport
***			<del> </del>			3.0
H0565	HUman Fetal Brain,	Human Fetal Brain				pCMVSport 2.0
IXOCCO	normalized 100024F	Uman Fatal Darin	<del> </del> -	<b></b>		pCMVSport
H0567	Human Fetal Brain, normalized A5002F	Human Fetal Brain				2.0
H0560	Human Fetal Brain.	Human Fetal Brain	<del> </del>	<del></del>	<del></del>	pCMVSport
H0569	normalized CO	numan retai Biain				2.0
H0571	Human Fetal Brain,	Human Fetal Brain	<del> </del>			pCMVSport
1103/1	normalized C500HE	, idina i cai maii		1		2.0
	Human Fetal Brain.	Human Fetal Brain				pCMVSport
H0572	Human retai brain.	Human retai brain	T .	li .		point appoin

H0574	Hepatocellular Tumor; re-	Hepatocellular	Liver		disease	Lambda
H0575	excision Human Adult	Tumor Human Adult	Lung		 	ZAP II Uni-ZAP XR
	Pulmonary;re-excision	Pulmonary				
H0576	Resting T-Cell; re- excision	T-Cells	Blood	Cell Line		Lambda ZAP II
H0578	Human Fetal Thymus	Fetal Thymus	Thymus			pSport1
H0579	Pericardium	Pericardium	Heart			pSport1
H0580	Dendritic cells, pooled	Pooled dendritic cells				pCMVSport 3.0
H0581	Human Bone Marrow, treated	Human Bone Marrow	Bone Marrow			pCMVSport 3.0
H0583	B Cell lymphoma	B Cell Lymphoma	B Cell		disease	pCMVSport 3.0
H0584	Activated T-cells, 24 hrs,re-excision	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0585	Activated T-Cells,12 hrs,re-excision	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0586	Healing groin wound, 6.5 hours post incision	healing groin wound, 6.5 hours post incision - 2/	groin		disease	pCMVSport 3.0
H0587	Healing groin wound; 7.5 hours post incision	Groin-2/19/97	groin		disease	pCMVSport 3.0
H0589	CD34 positive cells (cord blood),re-ex	CD34 Positive Cells	Cord Blood			ZAP Express
H0590	Human adult small intestine, re-excision	Human Adult Small Intestine	Small Int.			Uni-ZAP XR
H0591	Human T-cell lymphoma;re-excision	T-Cell Lymphoma	T-Cell		disease	Uni-ZAP XR
H0592	Healing groin wound - zero hr post-incision (control)	HGS wound healing project; abdomen			disease	pCMVSport 3.0
H0593	Olfactory epithelium;nasalcavity	Olfactory epithelium from roof of left nasal cacit				pCMVSport 3.0
H0594	Human Lung Cancer;re- excision	Human Lung Cancer	Lung		disease	Lambda ZAP II
H0595	Stomach cancer (human);re-excision	Stomach Cancer - 5383A (human)			disease	Uni-ZAP XR
H0596	Human Colon Cancer;re- excision	Human Colon Cancer	Colon			Lambda ZAP II
H0597	Human Colon; re-excision	Human Colon				Lambda ZAP II
H0598	Human Stomach;re- excision	Human Stomach	Stomach			Uni-ZAP XR
H0599	Human Adult Heart;re- excision	Human Adult Heart	Heart			Uni-ZAP XR
H0600	Healing Abdomen wound;70&90 min post incision	Abdomen			disease	pCMVSport 3.0
H0601	Healing Abdomen Wound;15 days post incision	Abdomen			disease	pCMVSport 3.0
H0602	Healing Abdomen Wound;21&29 days post incision	Abdomen			disease	pCMVSport 3.0
H0604	Human Pituitary, re- excision	Human Pituitary				pBluescript
H0606	Human Primary Breast Cancer;re-excision	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0608	H. Leukocytes, control	H.Leukocytes				pCMVSport
H0610	H. Leukocytes,	H.Leukocytes				pCMVSport

	normalized cot 5A		<del></del>	T	<del></del> _	T 1
H0611	H. Leukocytes,	H.Leukocytes	<del></del>	+		pCMVSport
	normalized cot 500 B	This call to your			]	pelvi v sport
H0612	H.Leukocytes, normalized cot 50 B	H.Leukocytes				pCMVSport
H0613	H.Leukocytes, normalized cot 5B	H.Leukocytes				pCMVSport
H0614	H. Leukocytes, normalized cot 500 A	H.Leukocytes				pCMVSport
H0615	Human Ovarian Cancer Reexcision	Ovarian Cancer	Ovary		disease	Uni-ZAP XR
H0616	Human Testes, Reexcision	Human Testes	Testis	<u> </u>		Uni-ZAP XR
H0617	Human Primary Breast Cancer Reexcision	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0618	Human Adult Testes, Large Inserts, Reexcision	Human Adult Testis	Testis			Uni-ZAP XR
H0619	Fetal Heart	Human Fetal Heart	Heart	<del> </del>		Uni-ZAP XR
H0620	Human Fetal Kidney; Reexcision	Human Fetal Kidney	Kidney			Uni-ZAP XR
H0622	Human Pancreas Tumor; Reexcision	Human Pancreas Tumor	Pancreas		disease	Uni-ZAP XR
H0623	Human Umbilical Vein;	Human Umbilical	Umbilical	1		Uni-ZAP XR
	Reexcision	Vein Endothelial Cells	vein			OIII-ZIII XXX
H0624	12 Week Early Stage Human II; Reexcision	Twelve Week Old Early Stage Human	Embryo			Uni-ZAP XR
H0625	Ku 812F Basophils Line	Ku 812F Basophils		1		pSport1
H0626	Saos2 Cells; Untreated	Saos2 Cell Line; Untreated				pSport1
H0627	Saos2 Cells; Vitamin D3 Treated	Saos2 Cell Line; Vitamin D3 Treated				pSport1
H0628	Human Pre-Differentiated Adipocytes	Human Pre- Differentiated	1			Uni-ZAP XR
H0629	Human Leukocyte, control #2	Adipocytes Human Normalized leukocyte				pCMVSport
H0631	Saos2, Dexamethosome Treated	Saos2 Cell Line; Dexamethosome Treated				pSport1
H0632	Hepatocellular Tumor;re- excision	Hepatocellular Tumor	Liver		-	Lambda ZAP H
H0633	Lung Carcinoma A549 TNFalpha activated	TNFalpha activated A549Lung Carcinoma	,		disease	pSport1
H0634	Human Testes Tumor, re- excision	Human Testes Tumor	Testis		disease	Uni-ZAP XR
H0635	Human Activated T-Cells, re-excision	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0637	Dendritic Cells From CD34 Cells	Dentritic cells from CD34 cells				pSport1
H0638	CD40 activated monocyte dendridic cells	CD40 activated monocyte dendridic cells				pSport1
H0639	Ficolled Human Stromal Cells, 5Fu treated	Ficolled Human Stromal Cells, 5Fu treated				Other
H0640	Ficolled Human Stromal Cells, Untreated	Ficolled Human Stromal Cells, Untreated				Other
H0641	LPS activated derived dendritic cells	LPS activated monocyte derived dendritic cells				pSport1
H0642	Hep G2 Cells, lambda	Hep G2 Cells		1		Other

	library				
H0643	Hep G2 Cells, PCR library	Hep G2 Cells			Other Uni-ZAP XR
H0644	Human Placenta (re- excision)	Human Placenta	Placenta		
H0645	Fetal Heart, re-excision	Human Fetal Heart	Heart		Uni-ZAP XR
H0646	Lung, Cancer (4005313 A3): Invasive Poorly Differentiated Lung Adenocarcinoma,	Metastatic squamous cell lung carcinoma, poorly di			pSport1
H0647	Lung, Cancer (4005163 B7): Invasive, Poorly Diff. Adenocarcinoma, Metastatic	Invasive poorly differentiated lung adenocarcinoma		disease	pSport1
H0648	Ovary, Cancer: (4004562 B6) Papillary Serous Cystic Neoplasm, Low Malignant Pot	Papillary Cstic neoplasm of low malignant potentia		disease	pSport1
H0649	Lung, Normal: (4005313 B1)	Normal Lung			pSport1
H0650	B-Cells	B-Cells			pCMVSport 3.0
H0651	Ovary, Normal: (9805C040R)	Normal Ovary			pSport1
H0652	Lung, Normal: (4005313 B1)	Normal Lung			pSport1
H0653	Stromal Cells	Stromal Cells			pSport1
H0654	Lung, Cancer: (4005313 A3) Invasive Poorly- differentiated Metastatic lung adenoc	Metastatic Squamous cell lung Carcinoma poorly dif			Other
H0656	B-cells (unstimulated)	B-cells (unstimulated)			pSport1
H0657	B-cells (stimulated)	B-cells (stimulated)			pSport1
H0658	Ovary, Cancer (9809C332): Poorly differentiated adenocarcinoma	9809C332- Poorly differentiate	Ovary & Fallopian Tub <b>e</b> s	disease	pSport1
H0659	Ovary, Cancer (15395A1F): Grade II Papillary Carcinoma	Grade II Papillary Carcinoma, Ovary	Ovary	disease	pSport1
H0660	Ovary, Cancer: (15799A1F) Poorly differentiated carcinoma	Poorly differentiated carcinoma, ovary		disease	pSport1
H0661	Breast, Cancer: (4004943 A5)	Breast cancer		disease	pSport1
H0662	Breast, Normal: (4005522B2)	Normal Breast - #4005522(B2)	Breast		pSport1
H0663	Breast, Cancer: (4005522 A2)	Breast Cancer - #4005522(A2)	Breast	disease	
H0664	Breast, Cancer: (9806C012R)	Breast Cancer	Breast	disease	
H0665	Stromal cells 3.88	Stromal cells 3.88		<del>                                     </del>	pSport1
H0666	Ovary, Cancer: (4004332 A2)	Ovarian Cancer, Sample #4004332A2		disease	
H0667	Stromal cells(HBM3.18)	Stromal cell(HBM 3.18)			pSport1
H0668	stromal cell clone 2.5	stromal cell clone 2.5			pSport1
H0669	Breast, Cancer: (4005385 A2)	Breast Cancer (4005385A2)	Breast		pSport1
H0670	Ovary, Cancer (4004650 A3): Well-Differentiated	Ovarian Cancer - 4004650A3			pSport1

<del></del>	Micropapillary Serous		-			
	Carcinoma					
H0671	Breast, Cancer: (9802C02OE)	Breast Cancer- Sample # 9802C02OE				pSport1
H0672	Ovary, Cancer: (4004576 A8)	Ovarian Cancer(4004576A8)	Ovary			pSport1
H0673	Human Prostate Cancer, Stage B2; re-excision	Human Prostate Cancer, stage B2	Prostate			Uni-ZAP XR
H0674	Human Prostate Cancer, Stage C; re-excission	Human Prostate Cancer, stage C	Prostate			Uni-ZAP XR
H0675	Colon, Cancer: (9808C064R)	Colon Cancer 9808C064R				pCMVSport 3.0
H0676	Colon, Cancer: (9808C064R)-total RNA	Colon Cancer 9808C064R				pCMVSport 3.0
H0677	TNFR degenerate oligo	B-Cells				PCRII
H0682	Serous Papillary Adenocarcinoma	serous papillary adenocarcinoma (9606G304SPA3B)				pCMVSport 3.0
H0683	Ovarian Serous Papillary Adenocarcinoma	Serous papillary adenocarcinoma, stage 3C (9804G01				pCMVSport 3.0
H0684	Serous Papillary Adenocarcinoma	Ovarian Cancer- 9810G606	Ovaries			pCMVSport 3.0
H0685	Adenocarcinoma of Ovary, Human Cell Line, # OVCAR-3	Adenocarcinoma of Ovary, Human Cell Line, # OVCAR-				pCMVSport 3.0
H0686	Adenocarcinoma of Ovary, Human Cell Line	Adenocarcinoma of Ovary, Human Cell Line, # SW-626				pCMVSport 3.0
H0687	Human normal ovary(#9610G215)	Human normal ovary(#9610G215)	Ovary			pCMVSport 3.0
H0688	Human Ovarian Cancer(#9807G017)	Human Ovarian cancer(#9807G017), mRNA from Maura Ru				pCMVSport 3.0
H0689	Ovarian Cancer	Ovarian Cancer, #9806G019				pCMVSport 3.0
H0690	Ovarian Cancer, # .9702G001	Ovarian Cancer, #9702G001				pCMVSport 3.0
H0691	Normal Ovary, #9710G208	normal ovary, #9710G208				pCMVSport 3.0
H0692	BLyS Receptor from Expression Cloning	B Cell Lymphoma	B Cell			pCMVSport 3.0
Н0693	Normal Prostate #ODQ3958EN	Normal Prostate Tissue # ODQ3958EN				pCMVSport 3.0
H0694	Prostate gland adenocarcinoma	Prostate gland, adenocarcinoma, mod/diff, gleason	prostate gland			pCMVSport 3.0
H0695	mononucleocytes from patient	mononucleocytes from patient at Shady Grove Hospit				pCMVSport 3.0
N0006	Human Fetal Brain	Human Fetal Brain				
N0007	Human Hippocampus	Human Hippocampus				
N0009	Human Hippocampus, prescreened	Human Hippocampus				
S0001	Brain frontal cortex	Brain frontal cortex	Brain			Lambda ZAP II
S0002	Monocyte activated	Monocyte-activated	blood	Cell Line		Uni-ZAP XR
S0003	Human Osteoclastoma	Osteoclastoma	bone	<b>- </b> -	disease	Uni-ZAP XR
S0004	Prostate	Prostate BPH	Prostate			Lambda

						ZAP II
S0006	Neuroblastoma	Human Neural Blastoma			disease	pCDNA
S0007	Early Stage Human Brain	Human Fetal Brain				Uni-ZAP XR
S0010	Human Amygdala	Amygdala				Uni-ZAP XR
S0011	STROMAL - OSTEOCLASTOMA	Osteoclastoma	bone		disease	Uni-ZAP XR
S0013	Prostate	Prostate	prostate			Uni-ZAP XR
S0015	Kidney medulla	Kidney medulla	Kidney			Uni-ZAP XR
S0016	Kidney Pyramids	Kidney pyramids	Kidney			Uni-ZAP XR
S0022	Human Osteoclastoma Stromal Cells - unamplified	Osteoclastoma Stromal Cells				Uni-ZAP XR
S0023	Human Kidney Cortex - unamplified	Human Kidney Cortex				-
S0026	Stromal cell TF274	stromal cell	Bone marrow	Cell Line		Uni-ZAP XR
S0027	Smooth muscle, serum treated	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XR
S0028	Smooth muscle,control	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XR
S0031	Spinal cord	Spinal cord	spinal cord			Uni-ZAP XR
S0032	Smooth muscle-ILb induced	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XR
S0036	Human Substantia Nigra	Human Substantia Nigra				Uni-ZAP XR
S0037	Smooth muscle, IL1b induced	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XR
S0038	Human Whole Brain #2 - Oligo dT > 1.5Kb	Human Whole Brain #2				ZAP Express
S0040	Adipocytes	Human Adipocytes from Osteoclastoma				Uni-ZAP XR
S0044	Prostate BPH	prostate BPH	Prostate		disease	Uni-ZAP XR
S0045	Endothelial cells-control	Endothelial cell	endothelial cell-lung	Cell Line		Uni-ZAP XR
S0046	Endothelial-induced	Endothelial cell	endothelial cell-lung	Cell Line		Uni-ZAP XR
S0048	Human Hypothalamus, Alzheimer"s	Human Hypothalamus, Alzheimer"s			disease	Uni-ZAP XR
S0049	Human Brain, Striatum	Human Brain, Striatum				Uni-ZAP XR
S0050	Human Frontal Cortex, Schizophrenia	Human Frontal Cortex, Schizophrenia			disease	Uni-ZAP XF
S0051	Human Hypothalmus,Schizophren ia	Human Hypothalamus, Schizophrenia			disease	Uni-ZAP XP
S0052	neutrophils control	human neutrophils	blood	Cell Line		Uni-ZAP XI
S0053	Neutrophils IL-1 and LPS induced	human neutrophil induced	blood	Cell Line		Uni-ZAP XF
S0106	STRIATUM DEPRESSION		BRAIN		disease	Uni-ZAP XI
S0110	Brain Amygdala Depression		Brain		disease	Uni-ZAP XI
S0112	Hypothalamus		Brain			Uni-ZAP XI
S0114	Anergic T-cell	Anergic T-cell		Cell Line		Uni-ZAP XI
S0114	Bone marrow	Bone marrow	Bone marrow			Uni-ZAP X
S0118	Smooth muscle control 2	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP X
S0126	Osteoblasts	Osteoblasts	Knee	Cell Line		Uni-ZAP X
S0120	Epithelial-TNFa and INF	Airway Epithelial	T	1		Uni-ZAP X
20152	induced					

S0134	Apoptotic T-cell	apoptotic cells		Cell Line		Uni-ZAP XR
S0136	PERM TF274	stromal cell	Bone marrow	Cell Line		Lambda
						ZAP II
S0140	eosinophil-IL5 induced	eosinophil	lung	Cell Line		Uni-ZAP XR
S0142	Macrophage-oxLDL	macrophage- oxidized LDL treated	blood	Cell Line		Uni-ZAP XR
S0144	Macrophage (GM-CSF treated)	Macrophage (GM- CSF treated)				Uni-ZAP XR
S0146	prostate-edited	prostate BPH	Prostate			Uni-ZAP XR
S0148	Normal Prostate	Prostate	prostate			Uni-ZAP XR
\$0150	LNCAP prostate cell line	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
S0152	PC3 Prostate cell line	PC3 prostate cell line				Uni-ZAP XR
S0168	Prostate/LNCAP, subtraction I	PC3 prostate cell line				pBluescript
S0176	Prostate, normal, subtraction I	Prostate	prostate			Uni-ZAP XR
S0180	Bone Marrow Stroma, TNF&LPS ind	Bone Marrow Stroma, TNF & LPS induced			disease	Uni-ZAP XR
S0182	Human B Cell 8866	Human B- Cell 8866		<b> </b>	11.	Uni-ZAP XR
S0188	Prostate,BPH, Lib 2	Human Prostate BPH			disease	pSport1
S0190	Prostate BPH,Lib 2, subtracted	Human Prostate BPH				pSport1
S0192	Synovial Fibroblasts (control)	Synovial Fibroblasts				pSport1
S0194	Synovial hypoxia	Synovial Fibroblasts				pSport1
S0196	Synovial IL-1/TNF stimulated	Synovial Fibroblasts				pSport1
S0206	Smooth Muscle- HASTE normalized	Smooth muscle	Pulmanary artery	Cell Line		pBluescript
S0208	Messangial cell, frac l	Messangial cell				pSport1
S0210	Messangial cell, frac 2	Messangial cell	<u> </u>	<b>_</b>		pSport1
S0212	Bone Marrow Stromal Cell, untreated	Bone Marrow Stromal Cell,untreated	_			pSportI
S0214	Human Osteoclastoma, re- excision	Osteoclastoma	bone		disease	Uni-ZAP XR
S0216	Neutrophils IL-1 and LPS induced	human neutrophil induced	blood	Cell Line		Uni-ZAP XR
S0218	Apoptotic T-cell, re-	apoptotic cells		Cell Line		Uni-ZAP XR
S0220	H. hypothalamus, frac A;re-excision	Hypothalamus	Brain			ZAP Express
S0222	H. Frontal cortex,epileptic;re- excision	H. Brain, Frontal Cortex, Epileptic	Brain		disease	Uni-ZAP XR
S0228	PSMIX	PBLS, 7TM receptor enriched				PCRII
S0238	PYFD	PYFD				PCRII
S0242	Synovial Fibroblasts (Il1/TNF), subt	Synovial Fibroblasts				pSport1
S0250	Human Osteoblasts II	Human Osteoblasts	Femur	-	disease	pCMVSport 2.0
S0252	7TM-PIMIX	PBLS, 7TM receptor enriched				PCRII
S0256	7TM-PHMIX	PBLS, 7TM receptor enriched				PCRII
S0258	7TM-PNMIX	PBLS, 7TM receptor enriched				PCRII

S0260	Spinal Cord, re-excision	Spinal cord	spinal cord			Uni-ZAP XR
S0266	PLMIX	PLMIX (Human	Lung			PCRII
		Lung)				
S0268	PRMIX	PRMIX (Human Prostate)	prostate			PCRII
S0270	PTMIX	PTMIX (Human Thymus)	Thymus			PCRII
\$0276	Synovial hypoxia-RSF subtracted	Synovial fobroblasts (rheumatoid)	Synovial tissue			pSport1
S0278	H Macrophage (GM-CSF treated), re-excision	Macrophage (GM- CSF treated)				Uni-ZAP XR
S0280	Human Adipose Tissue,	Human Adipose Tissue				Uni-ZAP XR
S0282	Brain Frontal Cortex, re-	Brain frontal cortex	Brain			Lambda ZAP II
S0294	Larynx tumor	Larynx tumor	Larynx,vocal cord		discase	pSport1
S0300	Frontal lobe, dementia; re- excision	Frontal Lobe dementia/Alzheimer' 's	Brain			Uni-ZAP XR
S0306	Larynx normal #10 261- 273	Larynx normal				pSport1
S0308	Spleen/normal	Spleen normal				pSport1
S0310	Normal trachea	Normal trachea				pSport1
S0312	Human osteoarthritic;fraction II	Human osteoarthritic cartilage			disease	pSport1
S0314	Human osteoarthritis;fraction I	Human osteoarthritic cartilage			disease	pSport1
S0316	Human Normal Cartilage, Fraction I	Human Normal Cartilage				pSport1
S0318	Human Normal Cartilage Fraction II	Human Normal Cartilage				pSport1
S0324	Human Brain	Brain	Cerebellum			pSport1
S0328	Palate carcinoma	Palate carcinoma	Uvula		disease	pSport1
S0330	Palate normal	Palate normal	Uvula			pSport1
S0332	Pharynx carcinoma	Pharynx carcinoma	Hypopharynx			pSport1
S0334	Human Normal Cartilage Fraction III	Human Normal Cartilage				pSport1
S0336	Human Normal Cartilage Fraction IV	Human Normal Cartilage				pSport1
S0338	Human Osteoarthritic Cartilage Fraction III	Human osteoarthritic cartilage			disease	pSport1
S0342	Adipocytes;re-excision	Human Adipocytes from Osteoclastoma				Uni-ZAP XR
S0344	Macrophage-oxLDL; re- excision	macrophage- oxidized LDL treated	blood	Cell Line		Uni-ZAP XR
S0346	Human Amygdala;re- excision	Amygdala				Uni-ZAP XR
S0348	Cheek Carcinoma	Cheek Carcinoma			disease	pSport1
S0350	Pharynx Carcinoma	Pharynx carcinoma	Hypopharynx		disease	pSport1
S0354	Colon Normal II	Colon Normal	Colon			pSport1
S0356	Colon Carcinoma	Colon Carcinoma	Colon		disease	pSport1
S0358	Colon Normal III	Colon Normal	Colon		<del></del>	pSport1
S0360	Colon Tumor II	Colon Tumor	Colon		disease	pSport1
S0362	Human Gastrocnemius	Gastrocnemius muscle				pSport1
S0364	Human Quadriceps	Quadriceps muscle	ļ	ļ		pSport1
S0366	Human Soleus	Soleus Muscle	<u> </u>	<u> </u>	<u> </u>	pSport1

S0370	Larynx carcinoma II	Larynx carcinoma			disease	pSport1
S0370	Larynx carcinoma III	Larynx carcinoma			disease	pSport1
S0374	Normal colon	Normal colon	·····			pSport1
S0374	Colon Tumor	Colon Tumor			disease	pSport1
S0378	Pancreas normal PCA4	Pancreas Normal				pSport1
30378	No	PCA4 No		1 1		
S0380	Pancreas Tumor PCA4 Tu	Pancreas Tumor			disease	pSport1
50500	I dilordad Tallion I Orrivita	PCA4 Tu		{ L		
S0382	Larynx carcinoma IV	Larynx carcinoma			disease	pSport1
S0384	Tongue carcinoma	Tongue carcinoma			disease	pSport1
S0386	Human Whole Brain, re-	Whole brain	Brain			ZAP Express
00000	excision	11.000		<u> </u>		<u> </u>
S0388	Human	Human			disease	Uni-ZAP XR
00000	Hypothalamus,schizophre	Hypothalamus,		i i		•
	nia, re-excision	Schizophrenia				
S0390	Smooth muscle, control;	Smooth muscle	Pulmanary	Cell Line		Uni-ZAP XR
20270	re-excision		artery			
S0392	Salivary Gland	Salivary gland;		1		pSport1
		normal				
S0396	Uterus; normal	Uterus; normal				pSport1
S0400	Brain; normal	Brain; normal				pSport1
S0402	Adrenal Gland, normal	Adrenal gland;		[		pSport1
		normal				
S0404	Rectum normal	Rectum, normal				pSport1
S0406	Rectum tumour	Rectum tumour				pSport1
S0408	Colon, normal	Colon, normal				pSport1
S0410	Colon, tumour	Colon, tumour			<u></u>	pSport1
S0412	Temporal cortex-	Temporal cortex,		1	disease	Other
	Alzheizmer; subtracted	alzheimer				
S0414	Hippocampus, Alzheimer	Hippocampus,		1		Other
	Subtracted	Alzheimer		ì		İ
		Subtracted				G) (V/C
S0418	CHME Cell Line;treated 5	CHME Cell Line;		1	i	pCMVSport 3.0
	hrs	treated			<del> </del>	pSport1
S0420	CHME Cell	CHME Cell line,		1		ророги
	Line, untreated	untreatetd Mo7e Cell Line		<del> </del>		pCMVSport
S0422	Mo7e Cell Line GM-CSF	GM-CSF treated	ļ		}	3.0
	treated (1ng/ml)	(lng/ml)	}			1
	TO 1 Call Line CM CCF	TF-1 Cell Line	<del> </del>	<del>- </del>	<u> </u>	pSport1
S0424	TF-1 Cell Line GM-CSF Treated	GM-CSF Treated	]	ļ	}	1 1
50406		Monocyte-activated	blood	Cell Line		Uni-ZAP XR
S0426	Monocyte activated; re-	[VIOIIOCYIC-activated	1	002		ļ
00420	Neutrophils control; re-	human neutrophils	blood	Cell Line		Uni-ZAP XR
S0428	excision	numan neuropins				
50420	Aryepiglottis Normal	Aryepiglottis	<del> </del>	<del>                                     </del>		pSport1
S0430	W Achigiours Motima	Normal	ļ	1	j	
S0432	Sinus piniformis Tumour	Sinus piniformis				pSport1
30432	Silius pililiotinis Tunioui	Tumour	Į	Į	ľ	
S0434	Stomach Normal	Stomach Normal			disease	pSport1
S0434 S0436	Stomach Tumour	Stomach Tumour	† · · · · ·		disease	pSport1
S0438	Liver Normal Met5No	Liver Normal	1			pSport1
30430	Lives indinial mices in	Met5No	1			
S0440	Liver Tumour Met 5 Tu	Liver Tumour	1			pSport1
S0440	Colon Normal	Colon Normal	1			pSport1
S0442	Colon Tumor	Colon Tumour	1		disease	pSport1
S0446	Tongue Tumour	Tongue Tumour	<del> </del>	<del></del>		pSport1
S0448	Larynx Normal	Larynx Normal	1		1	pSport1
S0448 S0450	Larynx Normai  Larynx Tumour	Larynx Tumour	-			pSport1
	Thymus	Thymus	1		T	pSport1
S0452		Thyroid normal	<del> </del>		1	pSport1
S0458						

S0460	Thyroid Tumour	Thyroid Tumour				pSport1
S0462	Thyroid Thyroiditis	Thyroid Thyroiditis				pSport1
S0464	Larynx Normal	Larynx Normal				pSport1
S0466	Larynx Tumor	Larynx Tumor		<del></del>	disease	pSport1
S0468	Ea.hy.926 cell line	Ea.hy.926 cell line		<del>   </del>		pSporti
S0472	Lung Mesothelium	PYBT PYBT				pSport1
S0474	Human blood platelets	Platelets	Blood			Other
50474	Human blood platelets	Platelets	platelets			Office
S0665	Human Amygdala; re- excission	Amygdala				Uni-ZAP XR
S3012	Smooth Muscle Serum Treated, Norm	Smooth muscle	Pulmanary artery	Cell Line		pBluescript
S3014	Smooth muscle, serum induced,re-exc	Smooth muscle	Pulmanary artery	Cell Line		pBluescript
S3018	TH1 cells	THI cells				Uni-ZAP XR
S3020	TH2 cells	TH2 cells				Uni-ZAP XR
S6014	H. hypothalamus, frac A	Hypothalamus	Brain			ZAP Express
S6016	H. Frontal Cortex,	H. Brain, Frontal	Brain		disease	Uni-ZAP XR
	Epileptic	Cortex, Epileptic				<u> </u>
S6022	H. Adipose Tissue	Human Adipose Tissue				Uni-ZAP XR
S6024	Alzheimers, spongy change	Alzheimer"s/Spongy change	Brain		disease	Uni-ZAP XR
S6026	Frontal Lobe, Dementia	Frontal Lobe dementia/Alzheimer' 's	Brain			Uni-ZAP XR
S6028	Human Manic Depression Tissue	Human Manic depression tissue	Brain		disease	Uni-ZAP XR
T0001	Human Brown Fat	Brown Fat				pBluescript . SK-
T0002	Activated T-cells	Activated T-Cell, PBL fraction	Blood	Cell Line		pBluescript SK-
T0003	Human Fetal Lung	Human Fetal Lung				pBluescript SK-
T0004	Human White Fat	Human White Fat				pBluescript SK-
Т0006	Human Pineal Gland	Human Pinneal Gland				pBluescript SK-
T0008	Colorectal Tumor	Colorectal Tumor			disease	pBluescript SK-
T0010	Human Infant Brain	Human Infant Brain				Other
T0023	Human Pancreatic	Human Pancreatic	1		disease	pBluescript
	Carcinoma	Carcinoma				SK-
T0039	HSA 172 Cells	Human HSA172 cell line				pBluescript SK-
T0040	HSC172 cells	SA172 Cells				pBluescript SK-
T0041	Jurkat T-cell G1 phase	Jurkat T-cell				pBluescript SK-
T0042	Jurkat T-Cell, S phase	Jurkat T-Cell Line				pBluescript SK-
T0047	T lymphocytes >70	T lymphocytes > 70				pBluescript SK-
T0048	Human Aortic Endothelium	Human Aortic Endothilium				pBluescript SK-
T0049	Aorta endothelial cells + TNF-a	Aorta endothelial cells				pBluescript SK-
T0060	Human White Adipose	Human White Fat				pBluescript SK-
T0067	Human Thyroid	Human Thyroid				pBluescript SK-
T0068	Normal Ovary,	Normal Ovary,				pBluescript

	Premenopausal	Premenopausal			<u> </u>	SK-
T0069	Human Uterus, normal	Human Uterus,				pBluescript
	,	normal				SK-
T0071	Human Bone Marrow	Human Bone				pBluescript
	Transaction Transaction	Marrow				SK-
T0074	Human Adult Retina	Human Adult Retina		<del> </del>		pBluescriptl
20011	Tioman rount rectifia	Trainan Adam Reima		1		SK-
T0082	Human Adult Retina	Human Adult Retina		+		pBluescript
10002	Human Addit Ketina	Human Adult Retina				
TOORC	II.	<del>  ,,                                  </del>		<del> </del>	<del></del>	SK-
T0086	Human Pancreatic	Human Pancreatic		1	disease	pBluescript
mo	Carcinoma Screened	Carcinoma		<u> </u>		SK-
T0109	Human (HCC) cell line	l t				pBluescript
	liver (mouse) metastasis,	l i		1		SK-
	remake			ļ		
T0110	Human colon carcinoma			1		pBluescript
	(HCC) cell line, remake				L	SK-
T0112	Human (Caco-2) cell line,	}				pBluescript
	adenocarcinoma, colon					SK-
T0114	Human (Caco-2) cell line,					pBluescript
	adenocarcinoma, colon,	1 1		1	l	SK-
	remake					
T0115	Human Colon Carcinoma					pBluescript
	(HCC) cell line			1		SK-
L0002	Atrium cDNA library		<del> </del>	1		
	Human heart	i		1		
L0005	Clontech human aorta					
20005	polyA+ mRNA (#6572)	1		ı İ		1
L0015	Human	<del>                                     </del>		<del> </del>		
L0013	Human adult (K.Okubo)			<del>- </del>	<del></del>	<del> </del>
	Human adult (K.Okubo)			<del> </del>		ļ
L0022	Human adult lung 3"	1		1		1
T 0000	directed MboI cDNA			ļ		ļ
L0033	Human chromosome					1
	13q14 cDNA					
L0040	Human colon mucosa					<u> </u>
L0041	Human epidermal					1
	keratinocyte			<u> </u>		Ĺ
L0052	Human normalized K562-					
	cDNA			i		1
L0055	Human promyelocyte					
L0062	Human whole brain		·			
L0065	Liver HepG2 cell line.					
L0097	Subtracted human retinal					<del> </del>
2007.	pigment epithelium (RPE)	1				]
L0105	Human aorta polyA+	aorta		<del></del>		<del> </del>
20103	(TFujiwara)	aorta		1.		
L0109	Human brain cDNA	brain		<del></del>		
L0109	Human placenta cDNA	· · · · · · · · · · · · · · · · · · ·		-		<del> </del>
LU142	Auman placenta CDNA	placenta		1		
T 01 12	(TFujiwara)	ļ — <del>, , , —  </del>				<del> </del>
L0143	Human placenta polyA+	placenta		į į		
	(TFujiwara)	L		<b> </b>		<b></b>
L0149	DKFZphsnu1	subthalamic nucleus				ļ
L0151	Human testis (C. De	testis		1		
	Smet)					l
L0157	Human fetal brain		brain			1
	(TFujiwara)			<u> </u>		<u> </u>
L0163	Human heart cDNA		heart			
	(YNakamura)					1
L0179	Human lung	lung		GLC-82		
	adenocarcinoma (M.Wu)	adenocarcinoma				1
L0194	Human pancreatic cancer	pancreatic cancer		Patu		<del> </del>
	cell line Patu 8988t	, , , , , , , , , , , , , , , , , , , ,	•	8988t	1	

					derived
L0352	Normalized infant brain, Bento Soares				BA, M13- derived
L0355	P, Human foetal Brain Whole tissue				Bluescript
L0356	S, Human foetal Adrenals				Bluescript
L0359	X, Human Liver tissue				Bluescript KS II+
L0360	Y, Human Placenta tissue				Bluescript KS II-+
L0361	Stratagene ovary (#937217)		ovary		Bluescript SK
L0362	Stratagene ovarian cancer (#937219)				Bluescript SK-
L0363	NCI_CGAP_GC2	germ cell tumor			Bluescript SK-
L0364	NCI_CGAP_GC5	germ cell tumor			Bluescript SK-
L0366	Stratagene schizo brain S11	schizophrenic brain S-11 frontal lobe			Bluescript SK-
L0367	NCI_CGAP_Sch1	Schwannoma tumor			Bluescript SK-
L0368	NCI_CGAP_SS1	synovial sarcoma			Bluescript SK-
L0369	NCI_CGAP_AA1	adrenal adenoma	adrenal gland		Bluescript SK-
L0370	Johnston frontal cortex	pooled frontal lobe	brain		Bluescript SK-
L0371	NCI_CGAP_Br3	breast tumor	breast		Bluescript SK-
L0372	NCI_CGAP_Co12	colon tumor	colon		Bluescript SK-
L0373	NCI_CGAP_Col1	turnor	colon		Bluescript SK-
L0374	NCI_CGAP_Co2	tumor	colon		Bluescript SK-
L0375	NCI_CGAP_Kid6	kidney tumor	kidney	:	Bluescript SK-
L0376	NCI_CGAP_Lar1	larynx	larynx		Bluescript SK-
L0377	NCI_CGAP_HN2	squamous cell carcinoma from vocal cord	larynx		Bluescript SK-
L0378	NCI_CGAP_Lu1	lung tumor	lung		Bluescript SK-
L0379	NCI_CGAP_Lym3	lymphoma	lymph node		Bluescript SK-
L0381	NCI_CGAP_HN4	squamous cell carcinoma	pharynx		Bluescript SK-
L0382	NCI_CGAP_Pr25	epithelium (cell line)	prostate		Bluescript SK-
L0383	NCI_CGAP_Pr24	invasive tumor (cell line)	prostate		Bluescript SK-
L0384	NCI_CGAP_Pr23	prostate tumor	prostate		Bluescript SK-
L0386	NCI_CGAP_HN3	squamous cell carcinoma from base of tongue	tongue		Bluescript SK-
L0387	NCI_CGAP_GCB0	germinal center B- cells	tonsil		Bluescript SK-
L0388	NCI_CGAP_HN6	normal gingiva (cell line from			Bluescript SK-

		immortalized kerati			
L0389	NCI CGAP HN5	normal gingiva (cell			Bluescript
		line from primary		Í	SK-
		keratinocyt			
L0393	B, Human Liver tissue				gt11
L0406	b4HB3MA Cot14.5				Lafmid A
L0411	1-NIB				Lafmid BA
L0416	b4HB3MA-Cot0.38-HAP- B				Lafmid BA
L0419	b4HB3MA-				Lafmid BA
	Cot109+103+85-Bio			[_	
L0420	b4HB3MA-Cot109+103				Lafmid BA
7.0425	Bio				Lafmid BA
L0425	b4HB3MA-Cot18-Bio b4HB3MA-FT20%-Biotin				Lafmid BA
L0427					lafmid BA
L0435	Infant brain, LLNL array of Dr. M. Soares 1NIB				
L0438	normalized infant brain cDNA	total brain	brain		lafmid BA
L0439	Soares infant brain 1NIB		whole brain		Lafmid BA
L0441	2HB3MK				Lafmid BK
L0444	НВ3МК				Lafmid BK
L0448	3HFLSK20				Lafmid K
L0454	Clontech adult human fat cell library HL1108A				lambda gt10
L0455	Human retina.cDNA	retina	eye		lambda gt10
L0433	randomly primed	Tours		1	
	sublibrary			1	
L0456	Human retina cDNA	retina	eye		lambda gt10
20.00	Tsp509I-cleaved sublibrary				
L0462	WATM1	<del></del>			lambda gtl l
L0468	HE6W				lambda zap
L0408	Human fetal heart,	<del></del>			Lambda
LOTT	Lambda ZAP Express	)			ZAP Express
L0475	KG1-a Lambda Zap			KG1-a	Lambda Zap
	Express cDNA library				Express
	,				(Stratagene)
L0477	HPLA CCLee	placenta			Lambda
7.0400	D				ZAP II Lambda
L0480	Stratagene cat#937212	ł		ļ į	ZAP,
	(1992)				pBluescript
			į ,	ŀ	SK(-)
L0481	CD34+DIRECTIONAL				Lambda
	}	:			ZAPII
L0483	Human pancreatic islet				Lambda ZAPII
L0485	STRATAGENE Human	skalatal musaka	leg muscle		Lambda
L0485	skeletal muscle cDNA	skeletal muscle	leg muscle		ZAPII
	library, cat. #936215.				ZA II
L0493	NCI_CGAP_Ov26	papillary serous	ovary		pAMP1
1,0493	1101_00/11_0720	carcinoma	"""		Pr 11.11
L0497	NCI CGAP HSC4	CD34+, CD38- from	bone marrow		pAMP1
2047/	1,0,_00,4,100,	normal bone marrow		\ \ \	,
		donor	1		
L0498	NCI_CGAP_HSC3	CD34+, T negative,	bone marrow		pAMP1
		patient with chronic			
		myelogenou			
L0499	NCI_CGAP_HSC2	stem cell 34+/38+	bone marrow		pAMP1
L0500	NCI_CGAP_Brn20	oligodendroglioma	brain		pAMP1
L0501	NCI_CGAP_Brn21	oligodendroglioma	brain	<u> </u>	pAMP1

L0509	NCI_CGAP_Lu26	invasive adenocarcinoma	lung		pAMP1
L0510	NCI_CGAP_Ov33	borderline ovarian carcinoma	ovary		pAMP1
L0512	NCI_CGAP_Ov36	borderline ovarian carcinoma	ovary		pAMP1
L0513	NCI_CGAP_Ov37	early stage papillary serous carcinoma	ovary		pAMP1
L0515	NCI_CGAP_Ov32	papillary serous carcinoma	ovary		pAMP1
L0517	NCI CGAP_Pr1	Carcillottia			pAMP10
L0517	NCI CGAP Pr2				pAMP10
L0519	NCI CGAP Pr3				pAMP10
L0520	NCI_CGAP_Alv1	alveolar			pAMP10
20320	1,01_0011	rhabdomyosarcoma			
L0521	NCI_CGAP_Ewl	Ewing"s sarcoma			pAMP10
L0522	NCI CGAP_Kid1	kidney			pAMP10
L0523	NCI CGAP Lip2	liposarcoma			pAMP10
L0525	NCI CGAP Li2	liver			pAMP10
L0526	NCI_CGAP_Pr12	metastatic prostate	Į.		pAMP10
		bone lesion			pAMP10
L0527	NCI_CGAP_Ov2	ovary			pAMP10
L0528	NCI_CGAP_Pr5	prostate			pAMP10
L0529	NCI_CGAP_Pr6	prostate			pAMP10
L0530	NCI_CGAP_Pr8	prostate			pAMP10
L0532	NCI_CGAP_Thy1	thyroid			pAMP10
L0533	NCI_CGAP_HSC1	stem cells	bone marrow brain		pAMP10
L0534	Chromosome 7 Fetal	brain	brain		P12
L0535	Brain cDNA Library NCI_CGAP_Br5	infiltrating ductal	breast		pAMP10
L0538	NCI_CGAP_Ov5	normal surface epithelium	ovary		pAMP10
L0539	Chromosome 7 Placental	ериненин	placenta		pAMP10
L0541	cDNA Library NCI_CGAP_Pr7	low-grade prostatic	prostate		pAMP10
L0542	NCI_CGAP_Prl1	normal prostatic	prostate		pAMP10
L0543	NCI_CGAP_Pr9	normal prostatic epithelial cells	prostate		pAMP10
L0544	NCI_CGAP_Pr4	prostatic intraepithelial neoplasia - high grade	prostate		pAMP10
L0545	NCI_CGAP_Pr4.1	prostatic intraepithelial neoplasia - high grade	prostate		pAMP10
L0551	NCI_CGAP_HN7	normal squamous epithelium, floor of mouth			pAMP10
L0558	NCI_CGAP_Ov40	endometrioid ovarian metastasis	ovary		pAMP10
L0559	NCI_CGAP_Ov39	papillary serous ovarian metastasis	ovary		pAMP10
L0560	NCI_CGAP_HN12	moderate to poorly differentiated invasive carcino	tongue		pAMP10
L0561	NCI_CGAP_HN11	normal squamous	tongue		pAMP10
L0562	Chromosome 7 HeLa			HeLa cell	pAMP10

	cDNA Library			line; ATCC		
L0563	Human Bone Marrow Stromal Fibroblast	bone marrow				pBluescript
L0564	Jia bone marrow stroma	bone marrow stroma				pBluescript
L0565	Normal Human Trabecular Bone Cells	Bone	Hip			pBluescript
L0581	Stratagene liver (#937224)		liver			pBluescript SK
L0584	Stratagene cDNA library Human heart, cat#936208					pBluescript SK(+)
L0586	HTCDL1					pBluescript SK(-)
L0587	Stratagene colon HT29 (#937221)					pBluescript SK-
L0588	Stratagene endothelial cell 937223					pBluescript SK-
L0589	Stratagene fetal retina 937202					pBluescript SK-
L0590	Stratagene fibroblast (#937212)					pBluescript SK-
L0591	Stratagene HeLa cell s3 937216				Ļ	pBluescript SK-
L0592	Stratagene hNT neuron (#937233)					pBluescript SK-
L0593	Stratagene neuroepithelium (#937231)					pBluescript SK-
L0594	Stratagene neuroepithelium NT2RAMI 937234					pBluescript SK-
L0595	Stratagene NT2 neuronal precursor 937230	neuroepithelial cells	brain			pBluescript SK-
L0596	Stratagene colon (#937204)		colon			pBluescript SK-
L0597	Stratagene corneal stroma (#937222)		cornea			pBluescript SK-
L0598	Morton Fetal Cochlea	cochlea	ear			pBluescript SK-
L0599	Stratagene lung (#937210)		lung			pBluescript SK-
L0600	Weizmann Olfactory Epithelium	olfactory epithelium	nose			pBluescript SK-
L0601	Stratagene pancreas (#937208)		pancreas			pBluescript SK- pBluescript
L0602	Pancreatic Islet	pancreatic islet	pancreas			SK- pBluescript
L0603	Stratagene placenta (#937225)		placenta			SK- pBluescript
L0604	Stratagene muscle 937209	muscle	skeletal muscle			SK-
L0605	Stratagene fetal spleen (#937205)	fetal spleen	spleen			pBluescript SK-
L0606	NCI_CGAP_Lym5	follicular lymphoma	lymph node			pBluescript SK-
L0607	NCI_CGAP_Lym6	mantle cell lymphoma	lymph node	NOT ITES		pBluescript SK- pBluescript
L0608	Stratagene lung carcinoma 937218		lung	NCI-H69		SK-
L0609	Schiller astrocytoma	astrocytoma	brain			pBluescript SK- (Stratagene)
L0611	Schiller meningioma	meningioma	brain			pBluescript

					SK- (Stratagene)
L0612	Schiller	oligodendroglioma	brain		pBluescript SK-
	oligodendroglioma			1_	(Stratagene)
L0615	22 week old human fetal liver cDNA library				pBluescriptII SK(-)
L0617	Chromosome 22 exon				pBluescriptII KS+
L0618	Chromosome 9 exon				pBluescriptII KS+
L0622	нмі				pcDNAII (Invitrogen)
L0623	НМ3	pectoral muscle (after mastectomy)			pcDNAII (Invitrogen)
L0625	NCI_CGAP_AR1	bulk alveolar tumor			pCMV- SPORT2
L0626	NCI_CGAP_GC1	bulk germ cell seminoma			pCMV- SPORT2
L0627	NCI_CGAP_Co1	bulk tumor	colon		pCMV- SPORT2
L0628	NCI_CGAP_Ov1	ovary bulk tumor	ovary		pCMV- SPORT2
L0629	NCI_CGAP_Mel3	metastatic melanoma to bowel	bowel (skin primary)		pCMV- SPORT4
L0630	NCI_CGAP_CNS1	substantia nigra	brain		pCMV- SPORT4
L0631	NCI_CGAP_Br7		breast		pCMV- SPORT4
L0633	NCI_CGAP_Lu6	small cell carcinoma	lung		pCMV- SPORT4
L0634	NCI_CGAP_Ov8	serous adenocarcinoma	ovary		pCMV- SPORT4
L0635	NCI_CGAP_PNS1	dorsal root ganglion	peripheral nervous system		pCMV- SPORT4
L0636	NCI_CGAP_Pit1	four pooled pituitary adenomas	brain		pCMV- SPORT6
L0637	NCI_CGAP_Bm53	three pooled meningiomas	brain		pCMV- SPORT6
L0638	NCI_CGAP_Brn35	tumor, 5 pooled (see description)	brain		pCMV- SPORT6
L0639	NCI_CGAP_Bm52	tumor, 5 pooled (see description)	brain		pCMV- SPORT6
L0640	NCI_CGAP_Br18	four pooled high- grade tumors, including two prima	breast		pCMV- SPORT6
L0641	NCI_CGAP_Co17	juvenile granulosa tumor	colon		pCMV- SPORT6
L0642	NCI_CGAP_Co18	moderately differentiated adenocarcinoma	colon		pGMV- SPORT6
L0643	NCI_CGAP_Co19	moderately differentiated adenocarcinoma	colon		pCMV- SPORT6
L0644	NCI_CGAP_Co20	moderately differentiated adenocarcinoma	colon		pCMV- SPORT6
L0645	NCI_CGAP_Co21	moderately differentiated adenocarcinoma	colon		pCMV- SPORT6
L0646	NCI_CGAP_Co14	moderately- differentiated	colon		pCMV- SPORT6

		adenocarcinoma			
L0647	NCI CGAP Sar4	five pooled	connective		pCMV-
		sarcomas, including	tissue	1	SPORT6
	1	myxoid liposarcoma			
L0648	NCI CGAP Eso2	squamous cell	esophagus		pCMV-
		carcinoma			SPORT6
L0649	NCI_CGAP_GU1	2 pooled high-grade	genitourinary		pCMV-
		transitional cell	tract		SPORT6
		tumors			
L0650	NCI_CGAP_Kid13	2 pooled Wilms"	kidney		pCMV-
D0030	1101_00111_111013	tumors, one primary		į.	SPORT6
		and one metast			j j
L0651	NCI CGAP Kid8	renal cell tumor	kidney		pCMV-
1,0001	NCI_COM_KING	renut con tuniot	i.i.d.i.o.j		SPORT6
T 0662	NCI CGAP_Lu27	four pooled poorly-	lung		pCMV-
L0652	NCI_CGAF_Lu2/	differentiated	lung		SPORT6
		adenocarcinomas			
7.0.650	1101 CO 17 1 25		lung		pCMV-
L0653	NCI_CGAP_Lu28	two pooled	lung		SPORT6
	1	squamous cell		ł	or oreio
		carcinomas	1 - 111:		pCMV-
L0654	NCI_CGAP_Lu31		lung, cell line	)	SPORT6
L0655	NCI_CGAP_Lym12	lymphoma,	lymph node		pCMV- SPORT6
	1	follicular mixed			SPORTO .
		small and large cell			
L0656	NCI_CGAP_Ov38	normal epithelium	ovary	1	pCMV-
					SPORT6
L0657	NCI_CGAP_Ov23	tumor, 5 pooled (see	ovary		pCMV-
		description)			SPORT6
L0658	NCI CGAP Ov35	tumor, 5 pooled (see	ovary		pCMV-
		description)			SPORT6
L0659	NCI_CGAP_Pan1	adenocarcinoma	pancreas	ſ	pCMV-
					SPORT6_
L0661	NCI_CGAP_Mel15	malignant	skin		pCMV-
20001	1.0.200.1.2	melanoma,			SPORT6
		metastatic to lymph			
	1 .	node	!		
L0662	NCI_CGAP_Gas4	poorly differentiated	stomach		pCMV-
		adenocarcinoma			SPORT6
		with signet r	1		
L0663	NCI_CGAP_Ut2	moderately-	uterus		pCMV-
D0003	Noi_cora _ct	differentiated		ŀ	SPORT6
i		endometrial			1
<u> </u>		adenocarcino	1		
L0664	NCI CGAP_Ut3	poorly-differentiated	uterus		pCMV-
20004	1.55555	endometrial	1		SPORT6
l		adenocarcinoma,	1		
L0665	NCI CGAP_Ut4	serous papillary	uterus		pCMV-
1 20003	HOLCOM TOW	carcinoma, high		)	SPORT6
{	1	grade, 2 pooled t			
TOCCC	NCL CGAR TH	well-differentiated	uterus		pCMV-
L0666	NCI_CGAP_Ut1	endometrial	ateras		SPORT6
		adenocarcinoma, 7			
7.5.55	LIGHT COLD CO.		whole blood		pCMV-
L0667	NCI_CGAP_CML1	myeloid cells, 18 pooled CML cases,	Whole blood	1	SPORT6
]			1		
L		BCR/ABL rearra	<del> </del>	<del> </del>	pCR2.1
L0681	Stanley Frontal SN	frontal lobe (see	brain		(Invitrogen)
	individual	description)	<del> </del>	<del>   </del>	pCR2.1-
L0684	Stanley Frontal SB pool 1	frontal lobe (see	brain	1	TOPO
1		description)			
	<u> </u>			L	(Invitrogen)
L0695	Human Glialblastoma Cell		Brain	BT-325	PCRII,
	i	1	l .	1 1	Invitrogen

			<del></del>		
L0697	Testis 1				PGEM 5zf(+)
L0698	Testis 2				PGEM 5zf(+)
Y 0015	0 1 323		<del> </del>	<del></del>	pSPORT1
L0717 L0720	Gessler Wilms tumor PN001-Normal Human		prostate		pSport1
	Prostate				pT7T3-Pac
L0731	Soares_pregnant_uterus_ NbHPU		uterus		
L0738	Human colorectal cancer				pT7T3D
L0740	Soares melanocyte	melanocyte			pT7T3D
	2NbHM	•	1	ĺ	(Pharmacia)
			1		with a
			1		modified
			<del></del>		polylinker
L0741	Soares adult brain		brain		pT7T3D
	N2b4HB55Y		1		(Pharmacia) with a
			1		modified
			1		polylinker
			1		pT7T3D
L0742	Soares adult brain		brain		(Pharmacia)
	N2b5HB55Y		1		with a
					modified
	(				polylinker
L0743	Soares breast 2NbHBst		breast		pT7T3D
L0743	Soales bleast zivonost		) oreast		(Pharmacia)
					with a
	i i				modified
	<b>i</b>		1 ' 1		polylinker
L0744	Soares breast 3NbHBst		breast		pT7T3D
20711			1		(Pharmacia)
	<u> </u>			}	with a
	1		ł		modified
					polylinker
L0745	Soares retina N2b4HR	retina	eyê		pT7T3D (Pharmacia)
	1			1	with a
	]			Į į	modified
	1 .		_ <u> </u>		polylinker
7.05746	Soares retina N2b5HR		91/9	<del> </del>	pT7T3D
L0746	Soares retina N205FIR	retina	eye	\ \ \	(Pharmacia)
		7		<u> </u>	with a
ĺ		•		1	modified
				\	polylinker
L0747	Soares_fetal_heart_NbHH		heart		pT7T3D
	19W			1	(Pharmacia)
				1	with a
	l i		İ	1	modified
				<del>                                     </del>	polylinker
L0748	Soares fetal liver spleen		Liver and		pT7T3D
	INFLS		Spleen	1	(Pharmacia) with a
1	1				modified
	1				polylinker
T.0740	Corres fotal lives sules		Liver and	<del> </del>	pT7T3D
L0749	Soares_fetal_liver_spleen		Spleen		(Pharmacia)
	_INFLS_SI		opice.	1	with a
1	1				modified
]	1		1	1	polylinker
L0750	Soares_fetal_lung_NbHL1		lung		pT7T3D
23,30	9W			1	(Pharmacia)
Í	1		1	1	with a
l			1	l'	modified

<del></del> -	<del></del>				polylinker
L0751	Soares ovary tumor	ovarian tumor	ovary		pT7T3D
	NЪНОТ	İ		[	(Pharmacia)
		ŀ			with a
			ŀ		modified
					polylinker pT7T3D
L0752	Soares_parathyroid_tumor	parathyroid tumor	parathyroid	1	(Pharmacia)
	NbHPA		gland	]	(Pharmacia) with a
	l [—]			j	modified
					polylinker
			<del></del>		pT7T3D
L0753	Soares_pineal_gland_N3H		pineal gland		(Pharmacia)
	PG				with a
	. }				modified
					polylinker
			1	<del></del>	pT7T3D
L0754	Soares placenta Nb2HP		placenta	l l	(Pharmacia)
	i i				with a
	]			1	modified
	ļ			!	polylinker
			placenta	<del></del>	pT7T3D
L0755	Soares_placenta_8to9wee		piaceilia	1	(Pharmacia)
	ks_2NbHP8to9W			1	with a
	l i			1 1	modified
				١, ١	polylinker
1.0256	Soares_multiple_sclerosis	multiple sclerosis			pT7T3D
L0756	2NbHMSP	lesions	ł	1	(Pharmacia)
	_ZINDHIVISF	10010110	1	}	with a
				1	modified
			1	1 !	polylinker
					V TYPE
L0757	Soares_senescent_fibrobla	senescent fibroblast		1	pT7T3D
	sts NbHSF			1	(Pharmacia)
	_		1	1 1	with a
	1			) 1	modified polylinker
	1			1	V TYPE
			<u> </u>	<del> </del>	pT7T3D-Pac
L0758	Soares_testis_NHT	•		1	(Pharmacia)
	1		· ·	1	with a
	4		İ	1	modified
	1		l	1	polylinker
	G I Con . NIPOTI	ļ		1	pT7T3D-Pac
L0759	Soares_total_fetus_Nb2H			1 1	(Pharmacia)
1	F8_9w		1	1 1	with a
ļ				1 1	modified
		į	Ţ	1	polylinker
L0760	Barstead aorta HPLRB3	aorta	1		pT7T3D-Pac
20,00	Parsicus sonta III Dicos			[ ]	(Pharmacia)
				1 1	with a
		Ì	1	1	modified
1		J			polylinker
L0761	NCI_CGAP_CLL1	B-cell, chronic		1 1	pT7T3D-Pa (Pharmacia)
		lymphotic leukemia			(Pharmacia) with a
1		(	1		with a modified
1	İ				polylinker
					pT7T3D-Pa
L0762	NCI_CGAP_Br1.1	breast	1	1	(Pharmacia)
1	}		1		with a
	1		1	1	modified
1	}		}		polylinker
	NCI CGAP_Br2	breast	<del></del>	<del>- </del>	pT7T3D-Pa
L0763		nrager			1

				<del>,</del>	<del>,                                      </del>	r.:
,		j		1	Ì	(Pharmacia)
		1		1	1	with a modified
		Į.		{		1
1.0764	NOT COAD O				<del>}</del>	polylinker pT7T3D-Pac
L0764	NCI_CGAP_Co3	colon		1	1	(Pharmacia)
					}	with a
		<u> </u>		1		modified
		1		1		polylinker
L0765	NCI_CGAP_Co4	colon		}	<del> </del> -	pT7T3D-Pac
L0703	NCI_COAF_CO4	Colon		İ		(Pharmacia)
						with a
		1				modified
		1.		}	1.	polylinker
L0766	NCI_CGAP_GCB1	germinal center B				pT7T3D-Pac
L0700	NCI_COAL_OCBI	cell		ł		(Pharmacia)
'		1		ŀ		with a
		1		(		modified
'				ļ	Ì	polylinker
L0767	NCI_CGAP_GC3	pooled germ cell			-	pT7T3D-Pac
20701	1.101_00111_001	tumors		1	1	(Pharmacia)
				1	Ì	with a
		į į		1	l	modified
				l		polylinker_
L0768	NCI CGAP GC4	pooled germ cell		T		pT7T3D-Pac
		tumors		1	}	(Pharmacia)
				1	}	with a
	ļ	]			1	modified
				<u> </u>	ļ .	polylinker
L0769	NCI_CGAP_Brn25	anaplastic	brain	1	1	pT7T3D-Pac
		oligodendroglioma		1	1	(Pharmacia)
	[			1	1	with a
	ļ	1				modified
				<del> </del>	<del> </del>	polylinker
L0770	NCI_CGAP_Bm23	glioblastoma	brain	1	ł	pT7T3D-Pac
		(pooled)		1		(Pharmacia) with a
	ł.	[ [		1	1	modified
				}	1	polylinker
L0771	NCI_CGAP_Co8	adenocarcinoma	colon	<del></del>	<del> </del>	pT7T3D-Pac
L0//1	NCI_COAP_COS	adenocarcinoma	COIGH	1	ł	(Pharmacia)
	1	1				with a
	ì	1		į	Ì	modified
					Ì	polylinker
L0772	NCI_CGAP_Co10	colon tumor RER+	colon	<del></del>	<del> </del>	pT7T3D-Pac
DOTTE	1102_00111_0010		1	}	}	(Pharmacia)
	į			1	1	with a
	1	)			1	modified
				1		polylinker
L0773	NCI_CGAP_Co9	colon tumor RER+	colon			pT7T3D-Pac
		ļ .		ì		(Pharmacia)
				1	1	with a
			}	1	1	modified
L						polylinker
L0774	NCI_CGAP_Kid3		kidney	1	1	pT7T3D-Pac
			1	1		(Pharmacia)
Ì			İ	1		with a
				}	1	modified
						polylinker
L0775	NCI_CGAP_Kid5	2 pooled tumors	kidney	1		pT7T3D-Pac
		(clear cell type)	Į.	1		(Pharmacia)
ļ	1		}	1	1	with a
			1	İ	1	modified polylinker
1	l			J		1 boraturket

L0776	NCI CGAP_Lu5		1	r	mama p. m
L0776	NCI_COAP_LUS	carcinoid	lung		pT7T3D-Pac
				1	(Pharmacia) with a
1	1		1	1	modified
l	1				polyłinker
L0777	Soares_NhHMPu_S1	Pooled human	mixed (see		pT7T3D-Pac
]	Source_Filminin a_Sr	melanocyte, fetal	below)	<u> </u>	(Pharmacia)
	1	heart, and pregnant	) Octow)	1	with a
	1	nourt, and prognant	1	1	modified
					polylinker
L0778	Barstead pancreas		pancreas		pT7T3D-Pac
	HPLRB1		Parerous		(Pharmacia)
l				1 1	with a
l	ĺ		l	1	modified
l_	į		1		polylinker
L0779	Soares_NFL_T_GBC_S1		pooled		pT7T3D-Pac
		,	•	l l	(Pharmacia)
			ł	]	with a
	Í		,		modified
	}			<u>                                     </u>	polylinker
L0780	Soares_NSF_F8_9W_OT		pooled		pT7T3D-Pac
	_PA_P_S1		_		(Pharmacia)
1			1		with a
			1	1 1	modified
			<u> </u>		polylinker
L0782	NCI_CGAP_Pr21	normal prostate	prostate		pT7T3D-Pac
1					(Pharmacia)
ł	[				with a
ļ			!		modified
1.0000	Not coup pice				polylinker
L0783	NCI_CGAP_Pr22	normal prostate	prostate	1	pT7T3D-Pac
	·			İ	(Pharmacia)
					with a
	·				modified
L0784	NCI_CGAP_Lei2	leiomyosarcoma	soft tissue		polylinker pT7T3D-Pac
D0704	NCI_COAI_LEIZ	reioinyosaicoma	SOR USSUE	<b>!</b>	(Pharmacia)
				ŀ	with a
				ĺ	modified
	•	'	1	1	polylinker
L0785	Barstead spleen HPLRB2		spleen		pT7T3D-Pac
		1			(Pharmacia)
			ļ	ł d	with a
		·		<u> </u>	modified
					polylinker
L0786	Soares_NbHFB		whole brain		pT7T3D-Pac
			1		(Pharmacia)
					with a
	]			]	modified
					polylinker
L0787	NCI_CGAP_Sub1				pT7T3D-Pac
					(Pharmacia)
	1				with a
					modified
1.0700	NOL COAD S 10		ļ		polylinker
L0788	NCI_CGAP_Sub2				pT7T3D-Pac
		]	,		(Pharmacia)
					with a
	:		]		modified
T 0000	NOT COAD S 15				polylinker
L0789	NCI_CGAP_Sub3		}		pT7T3D-Pac
			]		(Pharmacia)
				}	with a modified
L	l	L	<u>'</u> _	ll	Tuodinea

			<del></del>	Г Т	polylinker
L0790	NCI_CGAP_Sub4			1	pT7T3D-Pac
				1	(Pharmacia)
				1	with a
		1	•	}	modified
					polylinker
L0791	NCI_CGAP_Sub5			1 1	pT7T3D-Pac
				1	(Pharmacia)
		1		1	with a
		[ ]		[	modified
7.0000	No. Colb al.			<del> </del>	polylinker
L0792	NCI_CGAP_Sub6	}		<u> </u>	pT7T3D-Pac
i		1			(Pharmacia) with a
	•	1		[	modified
		1		1	polylinker
L0793	NCI_CGAP_Sub7	<del>   </del>		<del> </del>	pT7T3D-Pac
L0193	NCI_COAF_S007			1	(Phannacia)
		1		1	with a
		}		1	modified
		1			polylinker
L0794	NCI CGAP GC6	pooled germ cell			pT7T3D-Pac
		tumors			(Pharmacia)
		)		]	with a
					modified
					polylinker
L0796	NCI_CGAP_Bm50	medulloblastoma	brain		pT7T3D-Pac
				1	(Pharmacia)
	•	1			with a
		1			modified
T 0000	NGL CCAR C-16	- alan tuman DED I		<del> </del>	polylinker
L0800	NCI_CGAP_Col6	colon tumor, RER+	colon.		pT7T3D-Pac (Pharmacia)
					with a
				1 1	modified
			i	1	polylinker
L0803	NCI CGAP Kidl1		kidney	<del> </del>	pT7T3D-Pac
20003	1101_00111_111011		, ,,,,,,,,		(Pharmacia)
					with a
					modified
	<u> </u>			ļ	polylinker
L0804	NCI_CGAP_Kid12	2 pooled tumors	kidney		pT7T3D-Pac
'		(clear cell type)		i i	(Pharmacia)
		· ·			with a
					modified
70		<del>                                     </del>			polylinker
L0805	NCI_CGAP_Lu24	carcinoid	lung		pT7T3D-Pac (Pharmacia)
				1 1	with a
				]	modified
					polylinker
L0806	NCI_CGAP_Lu19	squamous cell	lung	<del> </del>	pT7T3D-Pac
150000	TOT COULTRIES	carcinoma, poorly	Julis		(Pharmacia)
		differentiated (4		1	with a
					modified
	1				polylinker
L0807	NCI_CGAP_Ov18	fibrotheoma	ovary		pT7T3D-Pac
				1 ' 1	(Pharmacia)
	1				with a
)	1				modified
		<u> </u>			polylinker
L0808	Barstead prostate BPH		prostate		pT7T3D-Pac
	HPLRB4 1			1	(Pharmacia)
I	I .	l .	I	1	with a

					modified polylinker
L0809	NCI_CGAP_Pr28		prostate		pT7T3D-Pac (Pharmacia) with a modified polylinker
L2242	subtracted 3" EST library		pancreas	AsPC- 1(ATCC: CRL- 1682)	pUC18
L2251	Human fetal lung	Fetal lung			

## TABLE 5

OMIM	Description
Reference	11.1.601460
100710	Myasthenic syndrome, slow-channel congenital, 601462
103050	Autism, succinylpurinemic
103050	Adenylosuccinase deficiency
104770	Amyloidosis, secondary, susceptibility to
106165	Hypertension, essential, 145500
107280	Cerebrovascular disease, occlusive
107280	Alpha-1-antichymotrypsin deficiency
107300	Antithrombin III deficiency
107400	Emphysema
107400	Emphysema-cirrhosis
107670	Apolipoprotein A-II deficiency
107777	Diabetes insipidus, nephrogenic, autosomal recessive, 222000
108725	Atherosclerosis, susceptibility to
109690	Asthma, nocturnal, susceptibility to
109690	Obesity, susceptibility to
110700	Vivax malaria, susceptibility to
113721	Breast cancer
113900	Heart block, progressive familial, type I
114208	Malignant hyperthermia susceptibility 5, 601887
114208	Hypokalemic periodic paralysis, 170400
116806	Colorectal cancer
117700	[Hypoceruloplasminemia, hereditary]
117700	Hemosiderosis, systemic, due to aceruloplasminemia
119300	van der Woude syndrome
120120	Epidermolysis bullosa dystrophica, dominant, 131750
120120	Epidermolysis bullosa dystrophica, recessive, 226600
120120	Epidermolysis bullosa, pretibial, 131850
120260	Epiphyseal dysplasia, multiple, type 2, 600204
120436	Muir-Torre family cancer syndrome, 158320
120436	Turcot syndrome with glioblastoma, 276300
120436	Colorectal cancer, hereditary nonpolyposis, type 2
120620	SLE susceptibility
120620	CR1 deficiency
120700	C3 deficiency
120920	Measles, susceptibility to
120950	C8 deficiency, type I
120960	C8 deficiency, type II
122500	[Transcortin deficiency]
123101	Craniosynostosis, type 2
123829	Melanoma
123940	White sponge nevus, 193900

125264	124030	Parkinsonism, susceptibility to
125264   Leukemia, acute nonlymphocytic   126340   Xeroderma pigmentosum, group D, 278730   126391   DNA ligase I deficiency   129490   Ectodermal dysplasia-3, anhidrotic   130410   Glutaricaciduria, type IIB   130500   Elliptocytosis-1   131210   Atherosclerosis, susceptibility to   133171   [Erythrocytosis, familial], 133100   133200   Erythrokeratodermia variabilis   134370   Factor H deficiency   134370   Hemolytic-uremic syndrome, 235400   134370   Hemolytic-uremic syndrome, 235400   134570   Factor XIIIA deficiency   134580   Factor XIIIB deficiency   134580   Factor XIIIB deficiency   134580   Factor XIIIB deficiency   136324   [Fish-odor syndrome], 602079   136836   Fucosyltransferase-6 deficiency   136836   Fucosyltransferase-6 deficiency   138140   Glucose transport defect, blood-brain barrier   138190   Diabetes mellitus, noninsulin-dependent   138320   Hemolytic anemia due to glutathione peroxidase deficiency   138981   Pulmonary alveolar proteinosis, 265120   139350   Epidermolytic hyperkeratosis, 113800   141800   Methemoglobinemias, alpha-141800   Thalassemias, alpha-141800   Heinz body anemias, alpha-141800   Heinz body anemias   141850   Hemolytic increase   Hemolytic anemia   141850   Hemolytic increase   141850   Hemolytic increase   141850   Hemolytic increase   141850   Hemolytic increase   141850   Hemolytic increase   141850   Hemolytic increase   141850   Pseudohypoaldosteronism, type II		
126340   Xeroderma pigmentosum, group D, 278730     126391   DNA ligase I deficiency     129490   Ectodermal dysplasia-3, anhidrotic     130410   Glutaricaciduria, type IIB     130500   Elliptocytosis-1     131210   Atherosclerosis, susceptibility to     133171   [Erythrocytosis, familial], 133100     133170   Erythrokeratodermia variabilis     134370   Factor H deficiency     134370   Hemolytic-uremic syndrome, 235400     134370   Membroproliferative glomerulonephritis     134570   Factor XIIIA deficiency     134580   Factor XIIIB deficiency     134580   Factor XIIIB deficiency     134790   Hyperferritinemia-cataract syndrome, 600886     135940   Ichthyosis vulgaris, 146700     136132   Fish-odor syndrome], 602079     136836   Fucosyltransferase-6 deficiency     137600   Iridogoniodysgenesis syndrome     138140   Glucose transport defect, blood-brain barrier     138190   Diabetes mellitus, noninsulin-dependent     13820   Hemolytic anemia due to glutathione peroxidase deficiency     138570   Non-insulin dependent diabetes mellitus, susceptibility to     139350   Epidermolytic hyperkeratosis, 113800     139350   Keratoderma, palmoplantar, nonepidermolytic     141750   Alpha-thalassemia/mental retardation syndrome, type 1     141800   Thalassemia, alpha-     141800   Heinz body anemias, alpha-     141800   Heinz body anemias, alpha-     141800   Heinz body anemia     141850   Heinz body anemia     141850   Heinz body anemia     141850   Hyperparathyroidism-jaw tumor syndrome     145260   Pseudohypoaldosteronism, type II	· · · · · · · · · · · · · · · · · · ·	
126391   DNA ligase I deficiency     129490   Ectodermal dysplasia-3, anhidrotic     130410   Glutaricaciduria, type IIB     130500   Elliptocytosis-1     131210   Atherosclerosis, susceptibility to     133171   [Erythrocytosis, familial], 133100     133200   Erythrokeratodermia variabilis     134370   Factor H deficiency     134370   Hemolytic-uremic syndrome, 235400     134370   Membroproliferative glomerulonephritis     134570   Factor XIIIA deficiency     134580   Factor XIIIB deficiency     134790   Hyperferritinemia-cataract syndrome, 600886     135940   Ichthyosis vulgaris, 146700     136132   [Fish-odor syndrome], 602079     136836   Facosyltransferase-6 deficiency     137600   Iridogoniodysgenesis syndrome     138140   Glucose transport defect, blood-brain barrier     138190   Diabetes mellitus, noninsulin-dependent     13820   Hemolytic anemia due to glutathione peroxidase deficiency     138570   Non-insulin dependent diabetes mellitus, susceptibility to     138981   Pulmonary alveolar proteinosis, 265120     139350   Epidermolytic hyperkeratosis, 113800     139350   Epidermolytic hyperkeratosis, 113800     139350   Keratoderma, palmoplantar, nonepidermolytic     141750   Alpha-thalassemia/mental retardation syndrome, type 1     141800   Methemoglobinemias, alpha-     141800   Erythremias, alpha-     141800   Heinz body anemia     141850   Heinz body anemia     141850   Hemoglobin H disease     141850   Hemoglobin H disease     141850   Hypochromic microcytic anemia     145001   Hyperparathyroidism-jaw tumor syndrome     145260   Pseudohypoaldosteronism, type II		
129490   Ectodermal dysplasia-3, anhidrotic   130410   Glutaricaciduria, type IIB   130500   Elliptocytosis-1   131210   Atherosclerosis, susceptibility to   133171   [Erythrocytosis, familial], 133100   133200   Erythrokeratodermia variabilis   134370   Factor H deficiency   134370   Hemolytic-uremic syndrome, 235400   134370   Membroproliferative glomerulonephritis   134570   Factor XIIIB deficiency   134580   Factor XIIIB deficiency   134580   Factor XIIIB deficiency   134590   Hyperferritinemia-cataract syndrome, 600886   135940   Ichthyosis vulgaris, 146700   136132   [Fish-odor syndrome], 602079   136836   Fucosyltransferase-6 deficiency   137600   Iridogoniodysgenesis syndrome   138140   Glucose transport defect, blood-brain barrier   138190   Diabetes mellitus, noninsulin-dependent   138320   Hemolytic anemia due to glutathione peroxidase deficiency   138981   Pulmonary alveolar proteinosis, 265120   139350   Epidermolytic hyperkeratosis, 113800   139350   Keratoderma, palmoplantar, nonepidermolytic   141750   Alpha-thalassemia/mental retardation syndrome, type 1   141800   Methemoglobinemias, alpha-141800   Erythrewinas, alpha-141800   Heinz body anemia, alpha-141850   Heinz body anemia   141850   Hemoglobin H disease   141850   Hypochronic microcytic anemia   145001   Hyperparathyroidism-jaw tumor syndrome   145260   Pseudohypoaldosteronism, type II		
130410   Glutaricaciduria, type IIB     130500   Elliptocytosis-1     131210   Atherosclerosis, susceptibility to     1313171   [Erythrocytosis, familial], 133100     133200   Erythrokeratodermia variabilis     134370   Factor H deficiency     134370   Hemolytic-uremic syndrome, 235400     134370   Membroproliferative glomerulonephritis     134570   Factor XIIIA deficiency     134580   Factor XIIIB deficiency     134590   Hyperferritinemia-cataract syndrome, 600886     135940   Ichthyosis vulgaris, 146700     136132   [Fish-odor syndrome], 602079     136336   Fucosyltransferase-6 deficiency     137600   Iridogoniodysgenesis syndrome     138140   Glucose transport defect, blood-brain barrier     138190   Diabetes mellitus, noninsulin-dependent     138320   Hemolytic anemia due to glutathione peroxidase deficiency     138981   Pulmonary alveolar proteinosis, 265120     139350   Epidermolytic hyperkeratosis, 113800     139350   Keratoderma, palmoplantar, nonepidermolytic     141750   Alpha-thalassemia/mental retardation syndrome, type 1     141800   Methemoglobinemias, alpha-     141800   Heinz body anemia, alpha-     141850   Thalassemia, alpha-     141850   Heinz body anemia     141850   Hemoglobin H disease     141850   Hyperparathyroidism-jaw tumor syndrome     145260   Pseudohypoaldosteronism, type II		
130500   Elliptocytosis-1     131210   Atherosclerosis, susceptibility to     133171   [Erythrocytosis, familial], 133100     133200   Erythrokeratodermia variabilis     134370   Factor H deficiency     134370   Hemolytic-uremic syndrome, 235400     134370   Membroproliferative glomerulonephritis     134570   Factor XIIIA deficiency     134580   Factor XIIIB deficiency     134790   Hyperferritinemia-cataract syndrome, 600886     135940   Ichthyosis vulgaris, 146700     136132   [Fish-odor syndrome], 602079     136836   Fucosyltransferase-6 deficiency     137600   Iridogoniodysgenesis syndrome     138140   Glucose transport defect, blood-brain barrier     138190   Diabetes mellitus, noninsulin-dependent     138320   Hemolytic anemia due to glutathione peroxidase deficiency     138570   Non-insulin dependent diabetes mellitus, susceptibility to     138981   Pulmonary alveolar proteinosis, 265120     139350   Epidermolytic hyperkeratosis, 113800     139350   Keratoderma, palmoplantar, nonepidermolytic     141750   Alpha-thalassemia/mental retardation syndrome, type 1     141800   Thalassemias, alpha-     141800   Thalassemias, alpha-     141800   Heinz body anemias, alpha-     141850   Hyperparathyroidism-jaw tumor syndrome     141850   Hyperparathyroidism-jaw tumor syndrome     145260   Pseudohypoaldosteronism, type II		
Atherosclerosis, susceptibility to   133171   [Erythrocytosis, familial], 133100   Brythrokeratodermia variabilis   134370   Factor H deficiency   134370   Hemolytic-uremic syndrome, 235400   134370   Membroproliferative glomerulonephritis   134570   Factor XIIIA deficiency   134580   Factor XIIIB deficiency   134790   Hyperferritinemia-cataract syndrome, 600886   135940   Ichthyosis vulgaris, 146700   136132   [Fish-odor syndrome], 602079   136836   Fucosyltransferase-6 deficiency   137600   Iridogoniodysgenesis syndrome   138140   Glucose transport defect, blood-brain barrier   138190   Diabetes mellitus, noninsulin-dependent   138320   Hemolytic anemia due to glutathione peroxidase deficiency   138981   Pulmonary alveolar proteinosis, 265120   139350   Epidermolytic hyperkeratosis, 113800   Epidermolytic hyperkeratosis, 113800   Methemoglobinemias, alpha-141800   Thalassemias, alpha-141800   Heinz body anemias, alpha-141850   Heinz body anemias, alpha-141850   Heinz body anemias, alpha-141850   Heinz body anemias, alpha-141850   Hemoglobin H disease   Hypochromic microcytic anemia   145001   Hyperparathyroidism-jaw tumor syndrome   145260   Pseudohypoaldosteronism, type II		
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138140 Glucose transport defect, blood-brain barrier 138190 Diabetes mellitus, noninsulin-dependent 138320 Hemolytic anemia due to glutathione peroxidase deficiency 138570 Non-insulin dependent diabetes mellitus, susceptibility to 138981 Pulmonary alveolar proteinosis, 265120 139350 Epidermolytic hyperkeratosis, 113800 139350 Keratoderma, palmoplantar, nonepidermolytic 141750 Alpha-thalassemia/mental retardation syndrome, type 1 141800 Methemoglobinemias, alpha- 141800 Thalassemias, alpha- 141800 Erythremias, alpha- 141800 Heinz body anemias, alpha- 141850 Thalassemia, alpha- 141850 Erythrocytosis 141850 Heinz body anemia 141850 Hemoglobin H disease 141850 Hemoglobin H disease 141850 Hypochromic microcytic anemia 145001 Hyperparathyroidism-jaw tumor syndrome 145260 Pseudohypoaldosteronism, type II	136836	Fucosyltransferase-6 deficiency
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Non-insulin dependent diabetes mellitus, susceptibility to  138981 Pulmonary alveolar proteinosis, 265120  139350 Epidermolytic hyperkeratosis, 113800  139350 Keratoderma, palmoplantar, nonepidermolytic  141750 Alpha-thalassemia/mental retardation syndrome, type 1  141800 Methemoglobinemias, alpha-  141800 Thalassemias, alpha-  141800 Erythremias, alpha-  141800 Heinz body anemias, alpha-  141850 Thalassemia, alpha-  141850 Erythrocytosis  141850 Heinz body anemia  141850 Hemoglobin H disease  141850 Hypochromic microcytic anemia  145001 Hyperparathyroidism-jaw tumor syndrome  145260 Pseudohypoaldosteronism, type II	138190	Diabetes mellitus, noninsulin-dependent
Non-insulin dependent diabetes mellitus, susceptibility to  138981 Pulmonary alveolar proteinosis, 265120  139350 Epidermolytic hyperkeratosis, 113800  139350 Keratoderma, palmoplantar, nonepidermolytic  141750 Alpha-thalassemia/mental retardation syndrome, type 1  141800 Methemoglobinemias, alpha-  141800 Thalassemias, alpha-  141800 Erythremias, alpha-  141800 Heinz body anemias, alpha-  141850 Thalassemia, alpha-  141850 Erythrocytosis  141850 Heinz body anemia  141850 Hemoglobin H disease  141850 Hypochromic microcytic anemia  145001 Hyperparathyroidism-jaw tumor syndrome  145260 Pseudohypoaldosteronism, type II	138320	Hemolytic anemia due to glutathione peroxidase deficiency
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141800         Erythremias, alpha-           141800         Heinz body anemias, alpha-           141850         Thalassemia, alpha-           141850         Erythrocytosis           141850         Heinz body anemia           141850         Hemoglobin H disease           141850         Hypochromic microcytic anemia           145001         Hyperparathyroidism-jaw tumor syndrome           145260         Pseudohypoaldosteronism, type II	141800	Methemoglobinemias, alpha-
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141850       Hypochromic microcytic anemia         145001       Hyperparathyroidism-jaw tumor syndrome         145260       Pseudohypoaldosteronism, type Π	141850	Heinz body anemia
145001 Hyperparathyroidism-jaw tumor syndrome 145260 Pseudohypoaldosteronism, type II	141850	Hemoglobin H disease
145260 Pseudohypoaldosteronism, type II	141850	Hypochromic microcytic anemia
145260 Pseudohypoaldosteronism, type II	145001	
143981   Hypocaiciume nypereaicemia, type II	145981	Hypocalciuric hypercalcemia, type II
146790 Lupus nephritis, susceptibility to		
147141 Leukemia, acute lymphoblastic		
147570 Interferon, immune, deficiency		
147680 Severe combined immunodeficiency due to IL2 deficiency		
147730 Interleukin-2 receptor, alpha chain, deficiency of		

147781	Atopy, susceptibility to
148040	Epidermolysis bullosa simplex, Koebner, Dowling-Meara, and Weber-
	Cockayne types, 131900, 131760, 131800
148041	Pachyonychia congenita, Jadassohn-Lewandowsky type, 167200
148043	Meesmann corneal dystrophy, 122100
148070	Liver disease, susceptibility to, from hepatotoxins or viruses
150210	Lactoferrin-deficient neutrophils, 245480
150292	Epidermolysis bullosa, Herlitz junctional type, 226700
150310	Epidermolysis bullosa, Herlitz junctional type, 226700
150310	Epidermolysis bullosa, generalized atrophic benign, 226650
152445	Vohwinkel syndrome, 124500
152445	Erythrokeratoderma, progressive symmetric, 602036
156850	Cataract, congenital, with microphthalmia
157640	PEO with mitochondrial DNA deletions, type 1
159001	Muscular dystrophy, limb-girdle, type 1B
159440	Charcot-Marie-Tooth neuropathy-1B, 118200
159440	Dejerine-Sottas disease, myelin P-related, 145900
159440	
	Hypomyelination, congenital
160900	Myotonic dystrophy
164040	Leukemia, acute promyelocytic, NPM/RARA type
164953	Liposarcoma
168360	Paraneoplastic sensory neuropathy
168468	Metaphyseal chondrodysplasia, Murk Jansen type, 156400
169600	Hailey-Hailey disease
171760	Hypophosphatasia, adult, 146300
171760	Hypophosphatasia, infantile, 241500
172471	Glycogenosis, hepatic, autosomal
173610	Platelet alpha/delta storage pool deficiency
173850	Polio, susceptibility to
174000	Medullary cystic kidney disease, AD
174900	Polyposis, juvenile intestinal
176100	Porphyria cutanea tarda
176100	Porphyria, hepatoerythropoietic
178300	Ptosis, hereditary congenital, 1
179755	Renal cell carcinoma, papillary, 1
179820	[Hyperproreninemia]
180071	Retinitis pigmentosa, autosomal recessive
180250	Retinol binding protein, deficiency of
180380	Night blindness, congenital stationery, rhodopsin-related
180380	Retinitis pigmentosa, autosomal recessive
180380	Retinitis pigmentosa-4, autosomal dominant
181430	Scapuloperoneal syndrome, myopathic type
182280	Small-cell cancer of lung
182380	Glucose/galactose malabsorption
182381	Renal glucosuria, 253100
182860	Pyropoikilocytosis

193960	Cub amountagin vaccagiyya
182860	Spherocytosis, recessive
182860	Elliptocytosis-2
186580	Arthrocutaneouveal granulomatosis
186770	Leukemia, T-cell acute lymphocytic
186780	CD3, zeta chain, deficiency
186960	Leukemia/lymphoma, T-cell
187040	Leukemia-1, T-cell acute lymphoblastic
188070	Bleeding disorder due to defective thromboxane A2 receptor
188550	Thyroid papillary carcinoma
188826	Sorsby fundus dystrophy, 136900
189800	Preeclampsia/eclampsia
190000	Atransferrinemia
190040	Dermatofibrosarcoma protuberans
190040	Giant-cell fibroblastoma
190040	Meningioma, SIS-related
190182	Colon cancer
190182	Colorectal cancer, familial nonpolyposis, type 6
191030	Nemaline myopathy-1, 161800
191044	Cardiomyopathy, familial hypertrophic
191045	Cardiomyopathy, familial hypertrophic, 2, 115195
191092	Tuberous sclerosis-2
191315	Insensitivity to pain, congenital, with anhidrosis, 256800
192340	Diabetes insipidus, neurohypophyseal, 125700
203500	Alkaptonuria
208100	Arthrogryposis multiplex congenita, neurogenic
208250	Jacobs syndrome
217030	C3b inactivator deficiency
222900	Sucrose intolerance
227646	Fanconi anemia, type D
230000	Fucosidosis
230800	Gaucher disease
230800	Gaucher disease with cardiovascular calcification
231200	Bernard-Soulier syndrome
231550	Achalasia-addisonianism-alacrimia syndrome
232050	Propionicacidemia, type II or pccB type
233710	Chronic granulomatous disease due to deficiency of NCF-2
234200	Neurodegeneration with brain iron accumulation
236730	Urofacial syndrome
245200	Krabbe disease
246450	HMG-CoA lyase deficiency
246530	Leukotriene C4 synthase deficiency
247200	Miller-Dieker lissencephaly syndrome
248510	Mannosidosis, beta-
250100	Metachromatic leukodystrophy
250800	Methemoglobinemia, type I
250800	Methemoglobinemia, type II

050040	G GY
252940	Sanfilippo syndrome, type D
254210	Myasthenia gravis, familial infantile
255800	Schwartz-Jampel syndrome
256540	Galactosialidosis
258501	3-methylglutaconicaciduria, type III
261510	Pseudo-Zellweger syndrome
262850	Plasmin inhibitor deficiency
264700	Pseudo-vitamin D dependency rickets 1
266200	Anemia, hemolytic, due to PK deficiency
271245	Spinocerebellar ataxia-8, infantile, with sensory neuropathy
271900	Canavan disease
276901	Usher syndrome, type 2
276902	Usher syndrome, type 3
278000	Wolman disease
278000	Cholesteryl ester storage disease
300008	Nephrolithiasis, type I, 310468
300008	Proteinuria, low molecular weight, with hypercalciuric
	nephrocalcinosis
300008	Dent disease, 300009
300008	Hypophosphatemia, type III
300047	Mental retardation, X-linked 20
301000	Thrombocytopenia, X-linked, 313900
301000	Wiskott-Aldrich syndrome
301220	Partington syndrome II
301300	Anemia, sideroblastic/hypochromic
301830	Arthrogryposis, X-linked (spinal muscular atrophy, infantile, X-linked)
302350	Nance-Horan syndrome
305400	Aarskog-Scott syndrome
306400	Chronic granulomatous disease, X-linked
308300	Incontinentia pigmenti, sporadic type
309470	Mental retardation, X-linked, syndromic-3, with spastic diplegia
309500	Renpenning syndrome-1
309585	Mental retardation, X-linked, syndromic-6, with gynecomastia and
200610	obesity  Mental retardation, X-linked, syndromic-2, with dysmorphism and
309610	cerebral atrophy
311050	Optic atrophy, X-linked
311250	Ornithine transcarbamylase deficiency
312040	N syndrome, 310465
312610	Retinitis pigmentosa-3
314850	McLeod phenotype
600040	Colorectal cancer
600059	Retinitis pigmentosa-13
600095	Split hand/foot malformation, type 3
600101	Deafness, autosomal dominant 2

600105	Retinitis pigmentosa-12, autosomal recessive
600138	Retinitis pigmentosa-11
600140	Rubenstein-Taybi syndrome, 180849
600163	Long QT syndrome-3
600179	Leber congenital amaurosis, type I, 204000
600179	Ichthyosis bullosa of Siemens, 146800
·	Palmoplantar keratoderma, Bothnia type
600231	Polycystic kidney disease, infantile severe, with tuberous sclerosis
600273	
600281	Non-insulin-dependent diabetes mellitus, 125853
600281	MODY, type 1, 125850
600332	Rippling muscle disease-1
600334	Tibial muscular dystrophy
600511	Schizophrenia-3
600512	Epilepsy, partial
600536	Myopathy, congenital
600584	Atrial septal defect with atrioventricular conduction defects, 108900
600650	Myopathy due to CPT II deficiency, 255110
600650	CPT deficiency, hepatic, type II, 600649
600722	Ceroid lipofuscinosis, neuronal, variant juvenile type, with granular
	osmiophilic deposits
600722	Ceroid lipofuscinosis, neuronal-1, infantile, 256730
600759	Alzheimer disease-4
600808	Enuresis, nocturnal, 2
600835	AIDS, resistance to
600882	Charcot-Marie-Tooth neuropathy-2B
600897	Cataract, zonular pulverulent-1, 116200
600919	Long QT syndrome-4 with sinus bradycardia
600923	Porphyria variegata, 176200
600956	Persistent Mullerian duct syndrome, type II, 261550
600957	Persistent Mullerian duct syndrome, type I, 261550
600977	Cone dystrophy, progressive
600995	Nephrotic syndrome, idiopathic, steroid-resistant
601105	Pycnodysostosis, 265800
601107	Dubin-Johnson syndrome, 237500
601130	Tolbutamide poor metabolizer
601154	Cardiomyopathy, dilated, 1E
601199	Neonatal hyperparathyroidism, 239200
601199	Hypocalcemia, autosomal dominant, 601198
601199	Hypocalciuric hypercalcemia, type I, 145980
601202	Cataract, anterior polar-2
601238	Cerebellar ataxia, Cayman type
601284	Hereditary hemorrhagic telangiectasia-2, 600376
601313	Polycystic kidney disease, adult type I, 173900
601412	Deafness, autosomal dominant 7
601471	Moebius syndrome-2
601494	Cardiomyopathy, familial, dilated-2
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601518	Prostate cancer, hereditary, 1, 176807
601542	
<del></del>	Rieger syndrome, type 1, 180500
601545	Lissencephaly-1
601556	Spinocerebellar ataxia-1, 164400
601652	Glaucoma 1A, primary open angle, juvenile-onset, 137750
601682	Glaucoma 1C, primary open angle
601744	Systemic lupus erythematosus, susceptibility to, 1
601769	Osteoporosis, involutional
601769	Rickets, vitamin D-resistant, 277440
601777	Cone dystrophy, progressive
601785	Carbohydrate-deficient glycoprotein syndrome, type I, 212065
601841	Protein C inhibitor deficiency
601846	Muscular dystrophy with rimmed vacuoles
601928	Monilethrix, 158000
601975	Ectodermal dysplasia/skin fragility syndrome
602014	Hypomagnesemia with secondary hypocalcemia
602082	Corneal dystrophy, Thiel-Behnke type
602116	Glioma
602153	Monilethrix, 158000
602216	Peutz-Jeghers syndrome, 175200
602225	Cone-rod retinal dystrophy-2, 120970
602225	Leber congenital amaurosis, type III
602477	Febrile convulsions, familial, 2
602491	Hyperlipidemia, familial combined, 1

Polynucleotide and Polypeptide Variants

[89] The present invention is directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X or the complementary strand thereto, nucleotide sequences encoding the polypeptide of SEQ ID NO:Y, the nucleotide sequence of SEQ ID NO:X encoding the polypeptide sequence as defined in column 7 of Table 1A, nucleotide sequences encoding the polypeptide as defined in column 7 of Table 1A, the nucleotide sequence as defined in columns 8 and 9 of Table 2, nucleotide sequences encoding the polypeptide encoded by the nucleotide sequence as defined in columns 8 and 9 of Table 2, the nucleotide sequence as defined in column 6 of Table 1B, nucleotide sequences encoding the polypeptide encoded by the nucleotide sequence as defined in column 6 of Table 1B, the cDNA sequence contained in Clone ID NO:Z, and/or nucleotide sequences encoding the polypeptide encoded by the cDNA sequence contained in Clone ID NO:Z.

[90] The present invention also encompasses variants of the polypeptide sequence disclosed in SEQ ID NO:Y, the polypeptide sequence as defined in column 7 of Table 1A, a polypeptide sequence encoded by the polynucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the nucleotide sequence as defined in columns 8 and 9 of Table 2, a polypeptide sequence encoded by the nucleotide sequence as defined in column 6 of Table 1B, a polypeptide sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, and/or a polypeptide sequence encoded by the cDNA sequence contained in Clone ID NO:Z.

[91] "Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

Thus, one aspect of the invention provides an isolated nucleic acid molecule comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence described in SEQ ID NO:X or contained in the cDNA sequence of Clone ID NO:Z; (b) a nucleotide sequence in SEQ ID NO:X or the cDNA in Clone ID NO:Z which encodes the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (c) a nucleotide sequence in SEQ ID NO:X or the cDNA in Clone ID NO:Z which encodes a mature polypeptide; (d) a nucleotide sequence in SEQ ID NO:X or the cDNA sequence of Clone ID NO:Z, which encodes a biologically active fragment of a polypeptide;

(e) a nucleotide sequence in SEQ ID NO:X or the cDNA sequence of Clone ID NO:Z, which encodes an antigenic fragment of a polypeptide; (f) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (g) a nucleotide sequence encoding a mature polypeptide of the amino acid sequence of SEQ ID NO:Y or the amino acid sequence encoded by the cDNA in Clone ID NO:Z; (h) a nucleotide sequence encoding a biologically active fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (i) a nucleotide sequence encoding an antigenic fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; and (j) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), or (i) above.

The present invention is also directed to nucleic acid molecules which comprise, [93] or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), (i), or (j) above, the nucleotide coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence of the cDNA contained in Clone ID NO:Z or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA contained in Clone ID NO:Z, the nucleotide coding sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto, a nucleotide sequence encoding the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto, the nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto, a nucleotide sequence encoding the polypeptide encoded by the nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto, the nucleotide sequence in SEQ ID NO:X encoding the polypeptide sequence as defined in column 7 of Table 1A or the complementary strand thereto, nucleotide sequences encoding the polypeptide as defined in column 7 of Table 1A or the complementary strand thereto,

and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polynucleotides which hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides and nucleic acids.

In a preferred embodiment, the invention encompasses nucleic acid molecules which comprise, or alternatively, consist of a polynucleotide which hybridizes under stringent hybridization conditions, or alternatively, under lower stringency conditions, to a polynucleotide in (a), (b), (c), (d), (e), (f), (g), (h), or (i), above, as are polypeptides encoded by these polynucleotides. In another preferred embodiment, polynucleotides which hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions, or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

In another embodiment, the invention provides a purified protein comprising, or alternatively consisting of, a polypeptide having an amino acid sequence selected from the group consisting of: (a) the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (b) the amino acid sequence of a mature form of a polypeptide having the amino acid sequence of SEQ ID NO:Y or the amino acid sequence encoded by the cDNA in Clone ID NO:Z; (c) the amino acid sequence of a biologically active fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; and (d) the amino acid sequence of an antigenic fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Y.

The present invention is also directed to proteins which comprise, or alternatively consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, any of the amino acid sequences in (a), (b), (c), or (d), above, the amino acid sequence shown in SEQ ID NO:Y, the amino acid sequence encoded by the cDNA contained in Clone ID NO:Z, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B, the amino acid sequence as defined in column 7 of Table 1A, an amino acid sequence encoded by the nucleotide

sequence in SEQ ID NO:X, and an amino acid sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X. Fragments of these polypeptides are also provided (e.g., those fragments described herein). Further proteins encoded by polynucleotides which hybridize to the complement of the nucleic acid molecules encoding these amino acid sequences under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are the polynucleotides encoding these proteins.

[97] By a nucleic acid having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the nucleic acid is identical to the reference sequence except that the nucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence referred to in Table 1A or 2 as the ORF (open reading frame), or any fragment specified as described herein.

[98] As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is expressed as percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

[99] If the subject sequence is shorter than the query sequence because of 5' or 3'

deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

[100] For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

[101] By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to

5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

[102] As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence of a polypeptide referred to in Table 1A (e.g., the amino acid sequence identified in column 6) or Table 2 (e.g., the amino acid sequence of the polypeptide encoded by the polynucleotide sequence defined in columns 8 and 9 of Table 2) or a fragment thereof, the amino acid sequence of the polypeptide encoded by the polynucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment thereof, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X or a fragment thereof, or the amino acid sequence of the polypeptide encoded by cDNA contained in Clone ID NO:Z, or a fragment thereof, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci.6:237-245 (1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is expressed as percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

[103] If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding

subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C- terminal residues of the subject sequence.

[104] For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the Nterminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequnce are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

[105] The polynucleotide variants of the invention may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, polypeptide variants in which less than 50, less than 40, less than 30, less than 20, less than 10, or 5-50, 5-25, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a

variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as E. coli).

[106] Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985)). These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the polypeptide of the present invention without substantial loss of biological function. As an example, Ron et al. (J. Biol. Chem. 268: 2984-2988 (1993)) reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem. 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

[109] Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N-

or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

[110] Thus, the invention further includes polypeptide variants which show a functional activity (e.g., biological activity) of the polypeptides of the invention. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity.

The present application is directed to nucleic acid molecules at least 80%, 85%, [111]90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein, (e.g., encoding a polypeptide having the amino acid sequence of an N and/or C terminal deletion), irrespective of whether they encode a polypeptide having functional activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having functional activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe or a polymerase chain reaction (PCR) primer. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having functional activity include, inter alia, (1) isolating a gene or allelic or splice variants thereof in a cDNA library; (2) in situ hybridization (e.g., "FISH") to metaphase chromosomal spreads to provide precise chromosomal location of the gene, as described in Verma et al., Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York (1988); (3) Northern Blot analysis for detecting mRNA expression in specific tissues (e.g., normal or diseased tissues); and (4) in situ hybridization (e.g., histochemistry) for detecting mRNA expression in specific tissues (e.g., normal or diseased tissues).

Preferred, however, are nucleic acid molecules having sequences at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein, which do, in fact, encode a polypeptide having functional activity. By a polypeptide having "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide of the invention for binding) to an anti-polypeptide of the invention antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide of the invention.

[113] The functional activity of the polypeptides, and fragments, variants and derivatives of the invention, can be assayed by various methods.

[114] For example, in one embodiment where one is assaying for the ability to bind or compete with a full-length polypeptide of the present invention for binding to an anti-polypetide antibody, various immunoassays known in the art can be used, including but not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

[115] In another embodiment, where a ligand is identified, or the ability of a polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel chromatography, protein affinity chromatography, and affinity blotting. See generally, Phizicky et al., Microbiol. Rev. 59:94-123 (1995). In another embodiment, the ability of physiological correlates of a polypeptide of the present invention to bind to a substrate(s) of the polypeptide of the invention can be routinely assayed using techniques known in the art.

[116] In addition, assays described herein (see Examples) and otherwise known in the art may routinely be applied to measure the ability of polypeptides of the present invention and fragments, variants and derivatives thereof to elicit polypeptide related biological activity (either *in vitro* or *in vivo*). Other methods will be known to the skilled artisan and are within the scope of the invention.

[117] Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to, for

example, the nucleic acid sequence of the cDNA contained in Clone ID NO:Z, the nucleic acid sequence referred to in Table 1A (SEQ ID NO:X), the nucleic acid sequence disclosed in Table 2 (e.g., the nucleic acid sequence delineated in columns 8 and 9) or fragments thereof, will encode polypeptides "having functional activity." In fact, since degenerate variants of any of these nucleotide sequences all encode the same polypeptide, in many instances, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having functional activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

- [118] For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.
- [119] The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.
- [120] The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. See Cunningham and Wells, Science 244:1081-1085 (1989). The resulting mutant molecules can then be tested for biological activity.
- [121] As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For

example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly. Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitutions with one or more of the amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), (iv) fusion of the polypeptide with additional amino acids, such as, for example, an IgG Fc fusion region peptide, serum albumin (preferably human serum albumin) or a fragment thereof, or leader or secretory sequence, or a sequence facilitating purification, or (v) fusion of the polypeptide with another compound, such as albumin (including but not limited to recombinant albumin (see, e.g., U.S. Patent No. 5,876,969, issued March 2, 1999, EP Patent 0 413 622, and U.S. Patent No. 5,766,883, issued June 16, 1998, herein incorporated by reference in their entirety)). Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

[122] For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. See Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).

[123] A further embodiment of the invention relates to polypeptides which comprise the amino acid sequence of a polypeptide having an amino acid sequence which contains at least one amino acid substitution, but not more than 50 amino acid substitutions, even more preferably, not more than 40 amino acid substitutions, still more preferably, not more than 30 amino acid substitutions, and still even more preferably, not more than 20 amino acid

substitutions from a polypeptide sequence disclosed herein. Of course it is highly preferable for a polypeptide to have an amino acid sequence which comprises the amino acid sequence of a polypeptide of SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X, an amino acid sequence encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, an amino acid sequence encoded by the complement of SEQ ID NO:X, and/or an amino acid sequence encoded by cDNA contained in Clone ID NO:Z which contains, in order of ever-increasing preference, at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 amino acid substitutions.

[124] In specific embodiments, the polypeptides of the invention comprise, or alternatively, consist of, fragments or variants of a reference amino acid sequence selected from: (a) the amino acid sequence of SEQ ID NO:Y or fragments thereof (e.g., the mature form and/or other fragments described herein); (b) the amino acid sequence encoded by SEQ ID NO:X or fragments thereof; (c) the amino acid sequence encoded by the complement of SEQ ID NO:X or fragments thereof; (d) the amino acid sequence encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or fragments thereof; and (e) the amino acid sequence encoded by cDNA contained in Clone ID NO:Z or fragments thereof; wherein the fragments or variants have 1-5, 5-10, 5-25, 5-50, 10-50 or 50-150, amino acid residue additions, substitutions, and/or deletions when compared to the reference amino acid sequence. In preferred embodiments, the amino acid substitutions are conservative. Polynucleotides encoding these polypeptides are also encompassed by the invention.

## Polynucleotide and Polypeptide Fragments

[125] The present invention is also directed to polynucleotide fragments of the polynucleotides (nucleic acids) of the invention. In the present invention, a "polynucleotide fragment" refers to a polynucleotide having a nucleic acid sequence which, for example: is a portion of the cDNA contained in Clone ID NO:Z or the complementary strand thereto; is a portion of the polynucleotide sequence encoding the polypeptide encoded by the cDNA contained in Clone ID NO:Z or the complementary strand thereto; is a portion of a polynucleotide sequence encoding the amino acid sequence encoded by the region of SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto; is a portion of the polynucleotide sequence of SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto; is

SEQ ID NO:X or the complementary strand thereto; is a polynucleotide sequence encoding a portion of the polypeptide of SEQ ID NO:Y; is a polynucleotide sequence encoding a portion of a polypeptide encoded by SEQ ID NO:X; is a polynucleotide sequence encoding a portion of a polypeptide encoded by the complement of the polynucleotide sequence in SEQ ID NO:X; is a portion of a polynucleotide sequence encoding the amino acid sequence encoded by the region of SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto; or is a portion of the polynucleotide sequence of SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto.

The polynucleotide fragments of the invention are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt, at least about 50 nt, at least about 75 nt, or at least about 150 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in Clone ID NO:Z, or the nucleotide sequence shown in SEQ ID NO:X or the complementary stand thereto. In this context "about" includes the particularly recited value or a value larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. These nucleotide fragments have uses that include, but are not limited to, as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., at least 160, 170, 180, 190, 200, 250, 500, 600, 1000, or 2000 nucleotides in length) are also encompassed by the invention.

[127] Moreover, representative examples of polynucleotide fragments of the invention comprise, or alternatively consist of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 601-650, 651-700, 701-750, 751-800, 801-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, 3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-3950, 3951-4000, 4001-4050, 4051-4100, 4101-4150, 4151-4200, 4201-4250, 4251-4300, 4301-4350, 4351-

4400, 4401-4450, 4451-4500, 4501-4550, 4551-4600, 4601-4650, 4651-4700, 4701-4750, 4751-4800, 4801-4850, 4851-4900, 4901-4950, 4951-5000, 5001-5050, 5051-5100, 5101-5150, 5151-5200, 5201-5250, 5251-5300, 5301-5350, 5351-5400, 5401-5450, 5451-5500, 5501-5550, 5551-5600, 5601-5650, 5651-5700, 5701-5750, 5751-5800, 5801-5850, 5851-5900, 5901-5950, 5951-6000, 6001-6050, 6051-6100, 6101-6150, 6151-6200, 6201-6250, 6251-6300, 6301-6350, 6351-6400, 6401-6450, 6451-6500, 6501-6550, 6551-6600, 6601-6650, 6651-6700, 6701-6750, 6751-6800, 6801-6850, 6851-6900, 6901-6950, 6951-7000, 7001-7050, 7051-7100, 7101-7150, 7151-7200, 7201-7250, 7251-7300 or 7301 to the end of SEQ ID NO:X, or the complementary strand thereto. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity). More preferably, these polynucleotides can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

Further representative examples of polynucleotide fragments of the invention [128] comprise, or alternatively consist of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 601-650, 651-700, 701-750, 751-800, 801-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, 3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-3950, 3951-4000, 4001-4050, 4051-4100, 4101-4150, 4151-4200, 4201-4250, 4251-4300, 4301-4350, 4351-4400, 4401-4450, 4451-4500, 4501-4550, 4551-4600, 4601-4650, 4651-4700, 4701-4750, 4751-4800, 4801-4850, 4851-4900, 4901-4950, 4951-5000, 5001-5050, 5051-5100, 5101-5150, 5151-5200, 5201-5250, 5251-5300, 5301-5350, 5351-5400, 5401-5450, 5451-5500, 5501-5550, 5551-5600, 5601-5650, 5651-5700, 5701-5750, 5751-5800, 5801-5850, 5851-

5900, 5901-5950, 5951-6000, 6001-6050, 6051-6100, 6101-6150, 6151-6200, 6201-6250, 6251-6300, 6301-6350, 6351-6400, 6401-6450, 6451-6500, 6501-6550, 6551-6600, 6601-6650, 6651-6700, 6701-6750, 6751-6800, 6801-6850, 6851-6900, 6901-6950, 6951-7000, 7001-7050, 7051-7100, 7101-7150, 7151-7200, 7201-7250, 7251-7300 or 7301 to the end of the cDNA sequence contained in Clone ID NO:Z, or the complementary strand thereto. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity). More preferably, these polynucleotides can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

Moreover, representative examples of polynucleotide fragments of the invention [129] comprise, or alternatively consist of, a nucleic acid sequence comprising one, two, three, four, five, six, seven, eight, nine, ten, or more of the above described polynucleotide fragments of the invention in combination with a polynucleotide sequence delineated in Table 1B column 6. Additional, representative examples of polynucleotide fragments of the invention comprise, or alternatively consist of, a nucleic acid sequence comprising one, two, three, four, five, six, seven, eight, nine, ten, or more of the above described polynucleotide fragments of the invention in combination with a polynucleotide sequence further embodiments, the above-described polynucleotide fragments of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotide fragments of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that

bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

- [130] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more fragments of the sequences delineated in column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1B, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.
- [131] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more fragments of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.
- [132] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more fragments of the sequences delineated in the same row of column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.
- [133] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that

bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X (e.g., as described herein) are directly contiguous Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[136] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B is directly contiguous with the 5' 10 polynucleotides of the next sequential exon delineated in Table 1B, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower

stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In the present invention, a "polypeptide fragment" refers to an amino acid [137] sequence which is a portion of that contained in SEQ ID NO:Y, a portion of an amino acid sequence encoded by the portion of SEQ ID NO:X as defined in columnss 8 and 9 of Table 2, a portion of an amino acid sequence encoded by the polynucleotide sequence of SEQ ID NO:X, a portion of an amino acid sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, and/or a portion of an amino acid sequence encoded by the cDNA contained in Clone ID NO:Z. Protein (polypeptide) fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 101-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-640, 641-660, 661-680, 681-700, 701-720, 721-740, 741-760, 761-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981-1000, 1001-1020, 1021-1040, 1041-1060, 1061-1080, 1081-1100, 1101-1120, 1121-1140, 1141-1160, 1161-1180, 1181-1200, 1201-1220, 1221-1240, 1241-1260, 1261-1280, 1281-1300, 1301-1320, 1321-1340, 1341-1360, 1361-1380, 1381-1400, 1401-1420, 1421-1440, or 1441 to the end of the coding region of cDNA and SEQ ID NO: Y. In a preferred embodiment, polypeptide fragments of the invention include, for example, fragments comprising, or alternatively consisting of, from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 101-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-640, 641-660, 661-680, 681-700, 701-720, 721-740, 741-760, 761-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981-1000, 1001-1020, 1021-1040, 1041-1060, 1061-1080, 1081-1100, 1101-1120, 1121-1140, 1141-1160, 1161-1180, 1181-1200,

1201-1220, 1221-1240, 1241-1260, 1261-1280, 1281-1300, 1301-1320, 1321-1340, 1341-1360, 1361-1380, 1381-1400, 1401-1420, 1421-1440, or 1441 to the end of the coding region of SEQ ID NO:Y. Moreover, polypeptide fragments of the invention may be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges or values, or ranges or values larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes. Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

[138] Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

[139] Accordingly, polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotides encoding these polypeptide fragments are also preferred.

[140] The present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X or the complement thereof, a polypeptide encoded by

the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, a polypeptide encoded by the portion of SEQ ID NO:B as defined in column 6 of Table 1B, and/or a polypeptide encoded by the cDNA contained in Clone ID NO:Z). In particular, N-terminal deletions may be described by the general formula m-q, where q is a whole integer representing the total number of amino acid residues in a polypeptide of the invention (e.g., the polypeptide disclosed in SEQ ID NO:Y, or the polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2), and m is defined as any integer ranging from 2 to q-6. Polynucleotides encoding these polypeptides are also encompassed by the invention.

- [141] The present invention further provides polypeptides having one or more residues from the carboxy terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, a polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, and/or a polypeptide encoded by the cDNA contained in Clone ID NO:Z). In particular, C-terminal deletions may be described by the general formula 1-n, where n is any whole integer ranging from 6 to q-1, and where n corresponds to the position of amino acid residue in a polypeptide of the invention. Polynucleotides encoding these polypeptides are also encompassed by the invention.
- In addition, any of the above described N- or C-terminal deletions can be combined to produce a N- and C-terminal deleted polypeptide. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini, which may be described generally as having residues m-n of a polypeptide encoded by SEQ ID NO:X (e.g., including, but not limited to, the preferred polypeptide disclosed as SEQ ID NO:Y and the polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2), the cDNA contained in Clone ID NO:Z, and/or the complement thereof, where n and m are integers as described above. Polynucleotides encoding these polypeptides are also encompassed by the invention.
- Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example the ability of the shortened mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the

complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

[144] The present application is also directed to proteins containing polypeptides at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a polypeptide sequence set forth herein. In preferred embodiments, the application is directed to proteins containing polypeptides at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to polypeptides having the amino acid sequence of the specific N- and C-terminal deletions. Polynucleotides encoding these polypeptides are also encompassed by the invention.

[145] Any polypeptide sequence encoded by, for example, the polynucleotide sequences set forth as SEQ ID NO:X or the complement thereof, (presented, for example, in Tables 1A and 2), the cDNA contained in Clone ID NO:Z, or the polynucleotide sequence as defined in column 6 of Table 1B, may be analyzed to determine certain preferred regions of the polypeptide. For example, the amino acid sequence of a polypeptide encoded by a polynucleotide sequence of SEQ ID NO:X (e.g., the polypeptide of SEQ ID NO:Y and the polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2) or the cDNA contained in Clone ID NO:Z may be analyzed using the default parameters of the DNASTAR computer algorithm (DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715 USA; http://www.dnastar.com/).

[146] Polypeptide regions that may be routinely obtained using the DNASTAR computer algorithm include, but are not limited to, Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions; Chou-Fasman alpha-regions, beta-regions, and turn-regions; Kyte-Doolittle hydrophilic regions and hydrophobic regions; Eisenberg alpha-and beta-amphipathic regions; Karplus-Schulz flexible regions; Emini surface-forming regions; and Jameson-Wolf regions of high antigenic index. Among highly preferred polynucleotides of the invention in this regard are those that encode polypeptides comprising regions that combine several structural features, such as several (e.g., 1, 2, 3 or 4) of the features set out above.

Additionally, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Emini surface-forming regions, and Jameson-Wolf regions of high antigenic index (i.e., containing four or more contiguous amino acids having an antigenic index of greater than or equal to 1.5, as identified using the default parameters of the Jameson-Wolf program) can routinely be used to determine polypeptide regions that exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from data by DNASTAR analysis by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

[148] Preferred polypeptide fragments of the invention are fragments comprising, or alternatively, consisting of, an amino acid sequence that displays a functional activity (e.g. biological activity) of the polypeptide sequence of which the amino acid sequence is a fragment. By a polypeptide displaying a "functional activity" is meant a polypeptide capable of one or more known functional activities associated with a full-length protein, such as, for example, biological activity, antigenicity, immunogenicity, and/or multimerization, as described herein.

[149] Other preferred polypeptide fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

[150] In preferred embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the antigenic fragments of the polypeptide of SEQ ID NO:Y, or portions thereof. Polynucleotides encoding these polypeptides are also encompassed by the invention.

[151] The present invention encompasses polypeptides comprising, or alternatively consisting of, an epitope of: the polypeptide sequence shown in SEQ ID NO:Y; a polypeptide sequence encoded by SEQ ID NO:X or the complementary strand thereto; the polypeptide sequence encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2; the polypeptide sequence encoded by the portion of SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereto; the polypeptide sequence encoded by the cDNA contained in Clone ID NO:Z; or the polypeptide sequence encoded by a polynucleotide that hybridizes to the sequence of SEQ ID NO:X, the complement of the

sequence of SEQ ID NO:X, the complement of a portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, or the cDNA sequence contained in Clone ID NO:Z under stringent hybridization conditions or alternatively, under lower stringency hybridization as defined *supra*. The present invention further encompasses polynucleotide sequences encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:X, or a fragment thereof), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize to the complementary strand under stringent hybridization conditions or alternatively, under lower stringency hybridization conditions defined *supra*.

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an antibody response in an animal, as determined by any method known in the art, for example, by the methods for generating antibodies described *infra*. (See, for example, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983)). The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross- reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

[153] Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

[154] In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and, most preferably, between about 15 to about 30 amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic

epitopes disclosed herein, as well as portions thereof. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. Preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these antigenic epitopes. Antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe et al., Science 219:660-666 (1983)).

[155] Non-limiting examples of epitopes of polypeptides that can be used to generate antibodies of the invention include a polypeptide comprising, or alternatively consisting of, at least one, two, three, four, five, six or more of the portion(s) of SEO ID NO:Y specified in column 7 of Table 1A. These polypeptide fragments have been determined to bear antigenic epitopes of the proteins of the invention by the analysis of the Jameson-Wolf antigenic index which is included in the DNAStar suite of computer programs. By "comprise" it is intended that a polypeptide contains at least one, two, three, four, five, six or more of the portion(s) of SEQ ID NO:Y shown in column 7 of Table 1A, but it may contain additional flanking residues on either the amino or carboxyl termini of the recited Such additional flanking sequences are preferably sequences naturally found adjacent to the portion; i.e., contiguous sequence shown in SEQ ID NO:Y. The flanking sequence may, however, be sequences from a heterolgous polypeptide, such as from another protein described herein or from a heterologous polypeptide not described herein. In particular embodiments, epitope portions of a polypeptide of the invention comprise one, two, three, or more of the portions of SEQ ID NO:Y shown in column 7 of Table 1A.

[156] Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle et al., J. Gen. Virol. 66:2347-2354 (1985). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes. The polypeptides comprising one or more immunogenic epitopes may be presented for eliciting an antibody response together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse), or, if the polypeptide is of sufficient length (at least about 25 amino acids), the polypeptide may be presented without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

[157] Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, in vivo immunization, in vitro immunization, and phage display methods. See, e.g., Sutcliffe et al., supra; Wilson et al., supra, and Bittle et al., J. Gen. Virol., 66:2347-2354 (1985). If in vivo immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a carrier using a linker such as maleimidobenzoyl- Nhydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier- coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg of peptide or carrier protein and Freund's adjuvant or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of antipeptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

[158] As one of skill in the art will appreciate, and as discussed above, the polypeptides of the present invention (e.g., those comprising an immunogenic or antigenic epitope) can be fused to heterologous polypeptide sequences. For example, polypeptides of the present invention (including fragments or variants thereof), may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof, resulting in chimeric polypeptides. By way of another non-limiting example, polypeptides and/or antibodies of the present invention (including fragments or variants thereof) may be fused with albumin (including but not limited to recombinant human serum albumin or fragments or variants thereof (see, e.g., U.S. Patent No. 5,876,969, issued March 2, 1999, EP Patent 0 413 622, and U.S. Patent No. 5,766,883, issued June 16, 1998, herein incorporated by reference in their entirety)). In a preferred embodiment, polypeptides and/or antibodies of the present invention (including fragments or variants thereof) are fused with the mature form of human serum albumin (i.e.,

amino acids 1 – 585 of human serum albumin as shown in Figures 1 and 2 of EP Patent 0 322 094) which is herein incorporated by reference in its entirety. In another preferred embodiment, polypeptides and/or antibodies of the present invention (including fragments or variants thereof) are fused with polypeptide fragments comprising, or alternatively consisting of, amino acid residues 1-z of human serum albumin, where z is an integer from 369 to 419, as described in U.S. Patent 5,766,883 herein incorporated by reference in its entirety. Polypeptides and/or antibodies of the present invention (including fragments or variants thereof) may be fused to either the N- or C-terminal end of the heterologous protein (e.g., immunoglobulin Fc polypeptide or human serum albumin polypeptide). Polynucleotides encoding fusion proteins of the invention are also encompassed by the invention.

[159] Such fusion proteins as those described above may facilitate purification and may increase half-life in vivo. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. See, e.g., EP 394,827; Traunecker et al., Nature, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG fusion proteins that have a disulfidelinked dimeric structure due to the IgG portion desulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., J. Biochem., 270:3958-3964 (1995). Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin (HA) tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., 1991, Proc. Natl. Acad. Sci. USA 88:8972-897). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an aminoterminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto Ni2+ nitriloacetic acid-agarose column and histidine-tagged proteins can be selectively eluted with imidazole-containing buffers.

## Fusion Proteins

[160] Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, polypeptides of the present invention which are shown to be secreted can be used as targeting molecules once fused to other proteins.

[161] Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

[162] In certain preferred embodiments, proteins of the invention are fusion proteins comprising an amino acid sequence that is an N and/or C- terminal deletion of a polypeptide of the invention. In preferred embodiments, the invention is directed to a fusion protein comprising an amino acid sequence that is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a polypeptide sequence of the invention. Polynucleotides encoding these proteins are also encompassed by the invention.

[163] Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

[164] As one of skill in the art will appreciate that, as discussed above, polypeptides of the present invention, and epitope-bearing fragments thereof, can be combined with heterologous polypeptide sequences. For example, the polypeptides of the present invention may be fused with heterologous polypeptide sequences, for example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM) or portions thereof (CH1, CH2, CH3, and any

combination thereof, including both entire domains and portions thereof), or albumin (including, but not limited to, native or recombinant human albumin or fragments or variants thereof (see, e.g., U.S. Patent No. 5,876,969, issued March 2, 1999, EP Patent 0 413 622, and U.S. Patent No. 5,766,883, issued June 16, 1998, herein incorporated by reference in their entirety)), resulting in chimeric polypeptides. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties (EP-A 0232 262). Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).

[165] Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a polypeptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., Cell 37:767 (1984)).

[166] Additional fusion proteins of the invention may be generated through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to modulate the activities of polypeptides of the invention, such methods can be used to generate polypeptides with altered activity, as well as agonists and antagonists of the polypeptides. See, generally, U.S. Patent Nos. 5,605,793; 5,811,238; 5,830,721; 5,834,252; and 5,837,458, and Patten et al., Curr. Opinion Biotechnol. 8:724-33 (1997); Harayama, Trends Biotechnol. 16(2):76-82 (1998); Hansson, et al., J. Mol. Biol. 287:265-76 (1999);

and Lorenzo and Blasco, Biotechniques 24(2):308- 13 (1998) (each of these patents and publications are hereby incorporated by reference in its entirety). In one embodiment, alteration of polynucleotides corresponding to SEQ ID NO:X and the polypeptides encoded by these polynucleotides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments by homologous or site-specific recombination to generate variation in the polynucleotide sequence. In another embodiment, polynucleotides of the invention, or the encoded polypeptides, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of a polynucleotide encoding a polypeptide of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

[167] Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

## Recombinant and Synthetic Production of Polypeptides of the Invention

[168] The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by synthetic and recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

[169] The polynucleotides of the invention may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

[170] The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon

at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418, glutamine synthase, or neomycin resistance for eukaryotic cell culture, and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells (e.g., Saccharomyces cerevisiae or Pichia pastoris (ATCC Accession No. 201178)); insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalph, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, pPIC9K, and PAO815 (all available from Invitrogen, Carlbad, CA). Other suitable vectors will be readily apparent to the skilled artisan.

Vectors which use glutamine synthase (GS) or DHFR as the selectable markers can be amplified in the presence of the drugs methionine sulphoximine or methotrexate, respectively. An advantage of glutamine synthase based vectors are the availabilty of cell lines (e.g., the murine myeloma cell line, NS0) which are glutamine synthase negative. Glutamine synthase expression systems can also function in glutamine synthase expressing cells (e.g., Chinese Hamster Ovary (CHO) cells) by providing additional inhibitor to prevent the functioning of the endogenous gene. A glutamine synthase expression system and components thereof are detailed in PCT publications: WO87/04462; WO86/05807; WO89/01036; WO89/10404; and WO91/06657, which are hereby incorporated in their entireties by reference herein. Additionally, glutamine synthase expression vectors can be obtained from Lonza Biologics, Inc. (Portsmouth, NH). Expression and production of

monoclonal antibodies using a GS expression system in murine myeloma cells is described in Bebbington *et al.*, *Bio/technology* 10:169(1992) and in Biblia and Robinson *Biotechnol. Prog.* 11:1 (1995) which are herein incorporated by reference.

[174] The present invention also relates to host cells containing the above-described vector constructs described herein, and additionally encompasses host cells containing nucleotide sequences of the invention that are operably associated with one or more heterologous control regions (e.g., promoter and/or enhancer) using techniques known of in The host cell can be a higher eukaryotic cell, such as a mammalian cell (e.g., a human derived cell), or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. A host strain may be chosen which modulates the expression of the inserted gene sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus expression of the genetically engineered polypeptide may be controlled. Furthermore, different host cells have characteristics and specific mechanisms for the translational and post-translational processing and modification (e.g., phosphorylation, cleavage) of proteins. Appropriate cell lines can be chosen to ensure the desired modifications and processing of the foreign protein expressed.

[175] Introduction of the nucleic acids and nucleic acid constructs of the invention into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., the coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination (see, e.g., US Patent Number

5,641,670, issued June 24, 1997; International Publication Number WO 96/29411; International Publication Number WO 94/12650; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

[177] Polypeptides of the invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

[178] Polypeptides of the present invention can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

In one embodiment, the yeast *Pichia pastoris* is used to express polypeptides of the invention in a eukaryotic system. *Pichia pastoris* is a methylotrophic yeast which can metabolize methanol as its sole carbon source. A main step in the methanol metabolization pathway is the oxidation of methanol to formaldehyde using O₂. This reaction is catalyzed by the enzyme alcohol oxidase. In order to metabolize methanol as its sole carbon source, *Pichia pastoris* must generate high levels of alcohol oxidase due, in part, to the relatively low affinity of alcohol oxidase for O₂. Consequently, in a growth medium depending on methanol as a main carbon source, the promoter region of one of the two alcohol oxidase

genes (AOXI) is highly active. In the presence of methanol, alcohol oxidase produced from the AOXI gene comprises up to approximately 30% of the total soluble protein in Pichia pastoris. See Ellis, S.B., et al., Mol. Cell. Biol. 5:1111-21 (1985); Koutz, P.J, et al., Yeast 5:167-77 (1989); Tschopp, J.F., et al., Nucl. Acids Res. 15:3859-76 (1987). Thus, a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, under the transcriptional regulation of all or part of the AOXI regulatory sequence is expressed at exceptionally high levels in Pichia yeast grown in the presence of methanol.

- [180] In one example, the plasmid vector pPIC9K is used to express DNA encoding a polypeptide of the invention, as set forth herein, in a *Pichea* yeast system essentially as described in "*Pichia* Protocols: Methods in Molecular Biology," D.R. Higgins and J. Cregg, eds. The Humana Press, Totowa, NJ, 1998. This expression vector allows expression and secretion of a polypeptide of the invention by virtue of the strong *AOX1* promoter linked to the *Pichia pastoris* alkaline phosphatase (PHO) secretory signal peptide (i.e., leader) located upstream of a multiple cloning site.
- [181] Many other yeast vectors could be used in place of pPIC9K, such as, pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, and PAO815, as one skilled in the art would readily appreciate, as long as the proposed expression construct provides appropriately located signals for transcription, translation, secretion (if desired), and the like, including an in-frame AUG as required.
- [182] In another embodiment, high-level expression of a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, may be achieved by cloning the heterologous polynucleotide of the invention into an expression vector such as, for example, pGAPZ or pGAPZalpha, and growing the yeast culture in the absence of methanol.
- [183] In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with

polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

In addition, polypeptides of the invention can be chemically synthesized using [184]techniques known in the art (e.g., see Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman & Co., N.Y., and Hunkapiller et al., Nature, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the polypeptide sequence. Non-classical amino acids include, but are not limited to, to the Disomers of the common amino acids, 2.4-diaminobutyric acid, a-amino isobutyric acid, 4aminobutyric acid, Abu, 2-amino butyric acid, g-Abu, e-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, tbutylalanine, phenylglycine, cyclohexylalanine, b-alanine, fluoro-amino acids, designer amino acids such as b-methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

The invention encompasses polypeptides of the present invention which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH₄; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

[186] Additional post-translational modifications encompassed by the invention include, for example, e.g., N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of procaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

[187] Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include iodine (121 I, 123 I, 125 I, 131 I), carbon (14C), sulfur (35S), tritium (3H), indium (111 In, 112 In, 113 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In,

In specific embodiments, a polypeptide of the present invention or fragment or variant thereof is attached to macrocyclic chelators that associate with radiometal ions, including but not limited to, ¹⁷⁷Lu, ⁹⁰Y, ¹⁶⁶Ho, and ¹⁵³Sm, to polypeptides. In a preferred embodiment, the radiometal ion associated with the macrocyclic chelators is ¹¹¹In. another preferred embodiment, the radiometal ion associated with the macrocyclic chelator ⁹⁰Y. specific embodiments, the macrocyclic chelator is tetraazacyclododecane-N,N',N",N"'-tetraacetic acid (DOTA). In other specific embodiments, DOTA is attached to an antibody of the invention or fragment thereof via a linker molecule. Examples of linker molecules useful for conjugating DOTA to a polypeptide are commonly known in the art - see, for example, DeNardo et al., Clin Cancer Res. 4(10):2483-90 (1998); Peterson et al., Bioconjug. Chem. 10(4):553-7 (1999); and Zimmerman et al, Nucl. Med. Biol. 26(8):943-50 (1999); which are hereby incorporated by reference in their entirety.

[189] As mentioned, the proteins of the invention may be modified by either natural

processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Polypeptides of the invention may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

[190] Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

[191] The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for

ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog). For example, the polyethylene glycol may have an average molecular weight of about 200, 500, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, 9500, 10,000, 10,500, 11,000, 11,500, 12,000, 12,500, 13,000, 13,500, 14,000, 14,500, 15,000, 15,500, 16,000, 16,500, 17,000, 17,500, 18,000, 18,500, 19,000, 19,500, 20,000, 25,000, 30,000, 35,000, 40,000, 45,000, 50,000, 55,000, 60,000, 65,000, 70,000, 75,000, 80,000, 85,000, 90,000, 95,000, or 100,000 kDa.

[192] As noted above, the polyethylene glycol may have a branched structure. Branched polyethylene glycols are described, for example, in U.S. Patent No. 5,643,575; Morpurgo et al., Appl. Biochem. Biotechnol. 56:59-72 (1996); Vorobjev et al., Nucleosides Nucleotides 18:2745-2750 (1999); and Caliceti et al., Bioconjug. Chem. 10:638-646 (1999), the disclosures of each of which are incorporated herein by reference.

[193] The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art, such as, for example, the method disclosed in EP 0 401 384 (coupling PEG to G-CSF), herein incorporated by reference; see also Malik et al., Exp. Hematol. 20:1028-1035 (1992), reporting pegylation of GM-CSF using tresyl chloride. For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues glutamic acid residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

[194] As suggested above, polyethylene glycol may be attached to proteins via linkage to any of a number of amino acid residues. For example, polyethylene glycol can be linked to proteins via covalent bonds to lysine, histidine, aspartic acid, glutamic acid, or cysteine residues. One or more reaction chemistries may be employed to attach polyethylene glycol

to specific amino acid residues (e.g., lysine, histidine, aspartic acid, glutamic acid, or cysteine) of the protein or to more than one type of amino acid residue (e.g., lysine, histidine, aspartic acid, glutamic acid, cysteine and combinations thereof) of the protein.

Using polyethylene glycol as an illustration of the present composition, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the N-terminus modification may be accomplished by reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved.

[196] As indicated above, pegylation of the proteins of the invention may be accomplished by any number of means. For example, polyethylene glycol may be attached to the protein either directly or by an intervening linker. Linkerless systems for attaching polyethylene glycol to proteins are described in Delgado et al., Crit. Rev. Thera. Drug Carrier Sys. 9:249-304 (1992); Francis et al., Intern. J. of Hematol. 68:1-18 (1998); U.S. Patent No. 4,002,531; U.S. Patent No. 5,349,052; WO 95/06058; and WO 98/32466, the disclosures of each of which are incorporated herein by reference.

[197] One system for attaching polyethylene glycol directly to amino acid residues of proteins without an intervening linker employs tresylated MPEG, which is produced by the modification of monmethoxy polyethylene glycol (MPEG) using tresylchloride (ClSO₂CH₂CF₃). Upon reaction of protein with tresylated MPEG, polyethylene glycol is directly attached to amine groups of the protein. Thus, the invention includes protein-polyethylene glycol conjugates produced by reacting proteins of the invention with a polyethylene glycol molecule having a 2,2,2-trifluoreothane sulphonyl group.

[198] Polyethylene glycol can also be attached to proteins using a number of different intervening linkers. For example, U.S. Patent No. 5,612,460, the entire disclosure of which

is incorporated herein by reference, discloses urethane linkers for connecting polyethylene glycol to proteins. Protein-polyethylene glycol conjugates wherein the polyethylene glycol is attached to the protein by a linker can also be produced by reaction of proteins with compounds such MPEG-succinimidylsuccinate, MPEG activated with 1,1'-carbonyldiimidazole, MPEG-2,4,5-trichloropenylcarbonate, MPEG-pnitrophenolcarbonate, and various MPEG-succinate derivatives. A number of additional polyethylene glycol derivatives and reaction chemistries for attaching polyethylene glycol to proteins are described in International Publication No. WO 98/32466, the entire disclosure of which is incorporated herein by reference. Pegylated protein products produced using the reaction chemistries set out herein are included within the scope of the invention.

[199] The number of polyethylene glycol moieties attached to each protein of the invention (i.e., the degree of substitution) may also vary. For example, the pegylated proteins of the invention may be linked, on average, to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, or more polyethylene glycol molecules. Similarly, the average degree of substitution within ranges such as 1-3, 2-4, 3-5, 4-6, 5-7, 6-8, 7-9, 8-10, 9-11, 10-12, 11-13, 12-14, 13-15, 14-16, 15-17, 16-18, 17-19, or 18-20 polyethylene glycol moieties per protein molecule. Methods for determining the degree of substitution are discussed, for example, in Delgado et al., Crit. Rev. Thera. Drug Carrier Sys. 9:249-304 (1992).

[200] The polypeptides of the invention can be recovered and purified from chemical synthesis and recombinant cell cultures by standard methods which include, but are not limited to, ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification. Well known techniques for refolding protein may be employed to regenerate active conformation when the polypeptide is denatured during isolation and/or purification.

[201] The polypeptides of the invention may be in monomers or multimers (i.e., dimers, trimers, tetramers and higher multimers). Accordingly, the present invention relates to monomers and multimers of the polypeptides of the invention, their preparation, and compositions (preferably, Therapeutics) containing them. In specific embodiments, the polypeptides of the invention are monomers, dimers, trimers or tetramers. In additional

embodiments, the multimers of the invention are at least dimers, at least trimers, or at least tetramers.

[202] Multimers encompassed by the invention may be homomers or heteromers. As used herein, the term homomer refers to a multimer containing only polypeptides corresponding to a protein of the invention (e.g., the amino acid sequence of SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X or the complement of SEQ ID NO:X, the amino acid sequence encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, and/or an amino acid sequence encoded by cDNA contained in Clone ID NO:Z (including fragments, variants, splice variants, and fusion proteins, corresponding to these as described herein)). These homomers may contain polypeptides having identical or different amino acid sequences. In a specific embodiment, a homomer of the invention is a multimer containing only polypeptides having an identical amino acid sequence. In another specific embodiment, a homomer of the invention is a multimer containing polypeptides having different amino acid sequences. In specific embodiments, the multimer of the invention is a homodimer (e.g., containing two polypeptides having identical or different amino acid sequences) or a homotrimer (e.g., containing three polypeptides having identical and/or different amino acid sequences). In additional embodiments, the homomeric multimer of the invention is at least a homodimer, at least a homotrimer, or at least a homotetramer.

[203] As used herein, the term heteromer refers to a multimer containing one or more heterologous polypeptides (i.e., polypeptides of different proteins) in addition to the polypeptides of the invention. In a specific embodiment, the multimer of the invention is a heterodimer, a heterotrimer, or a heterotetramer. In additional embodiments, the heteromeric multimer of the invention is at least a heterodimer, at least a heterotrimer, or at least a heterotetramer.

[204] Multimers of the invention may be the result of hydrophobic, hydrophilic, ionic and/or covalent associations and/or may be indirectly linked by, for example, liposome formation. Thus, in one embodiment, multimers of the invention, such as, for example, homodimers or homotrimers, are formed when polypeptides of the invention contact one another in solution. In another embodiment, heteromultimers of the invention, such as, for example, heterotrimers or heterotetramers, are formed when polypeptides of the invention contact antibodies to the polypeptides of the invention (including antibodies to the heterologous polypeptide sequence in a fusion protein of the invention) in solution. In other

embodiments, multimers of the invention are formed by covalent associations with and/or between the polypeptides of the invention. Such covalent associations may involve one or more amino acid residues contained in the polypeptide sequence (e.g., that recited in SEQ ID NO:Y, encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, and/or encoded by the cDNA contained in Clone ID NO:Z). In one instance, the covalent associations are cross-linking between cysteine residues located within the polypeptide sequences which interact in the native (i.e., naturally occurring) polypeptide. In another instance, the covalent associations are the consequence of chemical or recombinant manipulation. Alternatively, such covalent associations may involve one or more amino acid residues contained in the heterologous polypeptide sequence in a fusion protein. In one example, covalent associations are between the heterologous sequence contained in a fusion protein of the invention (see, e.g., US Patent Number 5,478,925). In a specific example, the covalent associations are between the heterologous sequence contained in a Fc fusion protein of the invention (as described herein). In another specific example, covalent associations of fusion proteins of the invention are between heterologous polypeptide sequence from another protein that is capable of forming covalently associated multimers, such as for example, osteoprotegerin (see, e.g., International Publication NO: WO 98/49305, the contents of which are herein incorporated by reference in its entirety). In another embodiment, two or more polypeptides of the invention are joined through peptide linkers. Examples include those peptide linkers described in U.S. Pat. No. 5,073,627 (hereby incorporated by reference). Proteins comprising multiple polypeptides of the invention separated by peptide linkers may be produced using conventional recombinant DNA technology.

Another method for preparing multimer polypeptides of the invention involves use of polypeptides of the invention fused to a leucine zipper or isoleucine zipper polypeptide sequence. Leucine zipper and isoleucine zipper domains are polypeptides that promote multimerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., Science 240:1759, (1988)), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble multimeric proteins of the invention are those described in PCT application WO 94/10308, hereby incorporated by reference. Recombinant fusion proteins comprising a polypeptide of the

invention fused to a polypeptide sequence that dimerizes or trimerizes in solution are expressed in suitable host cells, and the resulting soluble multimeric fusion protein is recovered from the culture supernatant using techniques known in the art.

[206] Trimeric polypeptides of the invention may offer the advantage of enhanced biological activity. Preferred leucine zipper moieties and isoleucine moieties are those that preferentially form trimers. One example is a leucine zipper derived from lung surfactant protein D (SPD), as described in Hoppe et al. (FEBS Letters 344:191, (1994)) and in U.S. patent application Ser. No. 08/446,922, hereby incorporated by reference. Other peptides derived from naturally occurring trimeric proteins may be employed in preparing trimeric polypeptides of the invention.

[207] In another example, proteins of the invention are associated by interactions between Flag® polypeptide sequence contained in fusion proteins of the invention containing Flag® polypeptide sequence. In a further embodiment, proteins of the invention are associated by interactions between heterologous polypeptide sequence contained in Flag® fusion proteins of the invention and anti-Flag® antibody.

[208] The multimers of the invention may be generated using chemical techniques known in the art. For example, polypeptides desired to be contained in the multimers of the invention may be chemically cross-linked using linker molecules and linker molecule length optimization techniques known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, multimers of the invention may be generated using techniques known in the art to form one or more intermolecule cross-links between the cysteine residues located within the sequence of the polypeptides desired to be contained in the multimer (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Further, polypeptides of the invention may be routinely modified by the addition of cysteine or biotin to the Cterminus or N-terminus of the polypeptide and techniques known in the art may be applied to generate multimers containing one or more of these modified polypeptides (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, techniques known in the art may be applied to generate liposomes containing the polypeptide components desired to be contained in the multimer of the invention (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

[209] Alternatively, multimers of the invention may be generated using genetic engineering techniques known in the art. In one embodiment, polypeptides contained in multimers of the invention are produced recombinantly using fusion protein technology described herein or otherwise known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In a specific embodiment, polynucleotides coding for a homodimer of the invention are generated by ligating a polynucleotide sequence encoding a polypeptide of the invention to a sequence encoding a linker polypeptide and then further to a synthetic polynucleotide encoding the translated product of the polypeptide in the reverse orientation from the original C-terminus to the Nterminus (lacking the leader sequence) (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In another embodiment, recombinant techniques described herein or otherwise known in the art are applied to generate recombinant polypeptides of the invention which contain a transmembrane domain (or hydrophobic or signal peptide) and which can be incorporated by membrane reconstitution techniques into liposomes (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

## Antibodies

Further polypeptides of the invention relate to antibodies and T-cell antigen [210] receptors (TCR) which immunospecifically bind a polypeptide, polypeptide fragment, or variant of the invention (e.g., a polypeptide or fragment or variant of the amino acid sequence of SEQ ID NO:Y or a polypeptide encoded by the cDNA contained in Clone ID No:Z, and/or an epitope, of the present invention) as determined by immunoassays well known in the art for assaying specific antibody-antigen binding. Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), intracellularlymade antibodies (i.e., intrabodies), and epitope-binding fragments of any of the above. The term "antibody," as used herein, refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1,

IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule. In preferred embodiments, the immunoglobulin molecules of the invention are IgG1. In other preferred embodiments, the immunoglobulin molecules of the invention are IgG4.

[211] Most preferably the antibodies are human antigen-binding antibody fragments of the present invention and include, but are not limited to, Fab, Fab' and F(ab')2, Fd, singlechain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a VL or VH domain. Antigen-binding antibody fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, CH1, CH2, and CH3 domains. Also included in the invention are antigen-binding fragments also comprising any combination of variable region(s) with a hinge region, CH1, CH2, and CH3 domains. The antibodies of the invention may be from any animal origin including birds and mammals. Preferably, the antibodies are human, murine (e.g., mouse and rat), donkey, ship rabbit, goat, guinea pig, camel, horse, or chicken. As used herein, "human" antibodies include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described infra and, for example in, U.S. Patent No. 5,939,598 by Kucherlapati et al.

The antibodies of the present invention may be monospecific, bispecific, trispecific or of greater multispecificity. Multispecific antibodies may be specific for different epitopes of a polypeptide of the present invention or may be specific for both a polypeptide of the present invention as well as for a heterologous epitope, such as a heterologous polypeptide or solid support material. See, e.g., PCT publications WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt, et al., J. Immunol. 147:60-69 (1991); U.S. Patent Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920; 5,601,819; Kostelny et al., J. Immunol. 148:1547-1553 (1992).

[213] Antibodies of the present invention may be described or specified in terms of the epitope(s) or portion(s) of a polypeptide of the present invention which they recognize or specifically bind. The epitope(s) or polypeptide portion(s) may be specified as described herein, e.g., by N-terminal and C-terminal positions, or by size in contiguous amino acid residues, or listed in the Tables and Figures. Preferred epitopes of the invention include the predicted epitopes shown in column 7 of Table 1A, as well as polynucleotides that encode

these epitopes. Antibodies which specifically bind any epitope or polypeptide of the present invention may also be excluded. Therefore, the present invention includes antibodies that specifically bind polypeptides of the present invention, and allows for the exclusion of the same.

[214] Antibodies of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies that do not bind any other analog, ortholog, or homolog of a polypeptide of the present invention are included. Antibodies that bind polypeptides with at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, and at least 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In specific embodiments, antibodies of the present invention cross-react with murine, rat and/or rabbit homologs of human proteins and the corresponding epitopes thereof. Antibodies that do not bind polypeptides with less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, and less than 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In a specific embodiment, the above-described cross-reactivity is with respect to any single specific antigenic or immunogenic polypeptide, or combination(s) of 2, 3, 4, 5, or more of the specific antigenic and/or immunogenic polypeptides disclosed herein. Further included in the present invention are antibodies which bind polypeptides encoded by polynucleotides which hybridize to a polynucleotide of the present invention under stringent hybridization conditions (as described herein). Antibodies of the present invention may also be described or specified in terms of their binding affinity to a polypeptide of the invention. Preferred binding affinities include those with a dissociation constant or Kd less than 5 X 10⁻² M, 10⁻² M, 5 X 10⁻³ M, 10⁻³ M, 5 X 10⁻³  4  M,  $10^{-4}$  M,  $5 \times 10^{-5}$  M,  $10^{-5}$  M,  $5 \times 10^{-6}$  M,  $10^{-6}$  M,  $5 \times 10^{-7}$  M,  $10^{7}$  M,  $5 \times 10^{-8}$  M,  $10^{-8}$  M,  $5 \times 10^{-9} \text{ M}, 10^{-9} \text{ M}, 5 \times 10^{-10} \text{ M}, 10^{-10} \text{ M}, 5 \times 10^{-11} \text{ M}, 10^{-11} \text{ M}, 5 \times 10^{-12} \text{ M}, 10^{-12} \text{ M}, 5 \times 10^{-12} \text{ M}$  $10^{-13}$  M,  $10^{-13}$  M, 5 X  $10^{-14}$  M,  $10^{-14}$  M, 5 X  $10^{-15}$  M, or  $10^{-15}$  M.

[215] The invention also provides antibodies that competitively inhibit binding of an antibody to an epitope of the invention as determined by any method known in the art for determining competitive binding, for example, the immunoassays described herein. In preferred embodiments, the antibody competitively inhibits binding to the epitope by at

least 95%, at least 90%, at least 85 %, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50%.

[216] Antibodies of the present invention may act as agonists or antagonists of the polypeptides of the present invention. For example, the present invention includes antibodies which disrupt the receptor/ligand interactions with the polypeptides of the invention either partially or fully. Preferably, antibodies of the present invention bind an antigenic epitope disclosed herein, or a portion thereof. The invention features both receptor-specific antibodies and ligand-specific antibodies. The invention also features receptor-specific antibodies which do not prevent ligand binding but prevent receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. For example, receptor activation can be determined by detecting the phosphorylation (e.g., tyrosine or serine/threonine) of the receptor or its substrate by immunoprecipitation followed by western blot analysis (for example, as described supra). In specific embodiments, antibodies are provided that inhibit ligand activity or receptor activity by at least 95%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50% of the activity in absence of the antibody.

[217] The invention also features receptor-specific antibodies which both prevent ligand binding and receptor activation as well as antibodies that recognize the receptorligand complex, and, preferably, do not specifically recognize the unbound receptor or the unbound ligand. Likewise, included in the invention are neutralizing antibodies which bind the ligand and prevent binding of the ligand to the receptor, as well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor. Further included in the invention are antibodies which activate the receptor. These antibodies may act as receptor agonists, i.e., potentiate or activate either all or a subset of the biological activities of the ligand-mediated receptor activation, for example, by inducing dimerization of the receptor. The antibodies may be specified as agonists, antagonists or inverse agonists for biological activities comprising the specific biological activities of the peptides of the invention disclosed herein. The above antibody agonists can be made using methods known in the art. See, e.g., PCT publication WO 96/40281; U.S. Patent No. 5,811,097; Deng et al., Blood 92(6):1981-1988 (1998); Chen et al., Cancer Res. 58(16):3668-3678 (1998); Harrop et al., J. Immunol. 161(4):1786-1794 (1998); Zhu et al., Cancer Res. 58(15):3209-3214 (1998); Yoon et al., J. Immunol.

160(7):3170-3179 (1998); Prat et al., J. Cell. Sci. 111(Pt2):237-247 (1998); Pitard et al., J. Immunol. Methods 205(2):177-190 (1997); Liautard et al., Cytokine 9(4):233-241 (1997); Carlson et al., J. Biol. Chem. 272(17):11295-11301 (1997); Taryman et al., Neuron 14(4):755-762 (1995); Muller et al., Structure 6(9):1153-1167 (1998); Bartunek et al., Cytokine 8(1):14-20 (1996) (which are all incorporated by reference herein in their entireties).

[218] Antibodies of the present invention may be used, for example, to purify, detect, and target the polypeptides of the present invention, including both in vitro and in vivo diagnostic and therapeutic methods. For example, the antibodies have utility in immunoassays for qualitatively and quantitatively measuring levels of the polypeptides of the present invention in biological samples. See, e.g., Harlow et al., Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); incorporated by reference herein in its entirety.

[219] As discussed in more detail below, the antibodies of the present invention may be used either alone or in combination with other compositions. The antibodies may further be recombinantly fused to a heterologous polypeptide at the N- or C-terminus or chemically conjugated (including covalent and non-covalent conjugations) to polypeptides or other compositions. For example, antibodies of the present invention may be recombinantly fused or conjugated to molecules useful as labels in detection assays and effector molecules such as heterologous polypeptides, drugs, radionuclides, or toxins. See, e.g., PCT publications WO 92/08495; WO 91/14438; WO 89/12624; U.S. Patent No. 5,314,995; and EP 396,387; the disclosures of which are incorporated herein by reference in their entireties.

The antibodies of the invention include derivatives that are modified, i.e, by the covalent attachment of any type of molecule to the antibody such that covalent attachment does not prevent the antibody from generating an anti-idiotypic response. For example, but not by way of limitation, the antibody derivatives include antibodies that have been modified, e.g., by glycosylation, acetylation, pegylation, phosphylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Additionally, the derivative may contain one or more non-classical amino acids.

The antibodies of the present invention may be generated by any suitable method known in the art. Polyclonal antibodies to an antigen-of- interest can be produced by various procedures well known in the art. For example, a polypeptide of the invention can be administered to various host animals including, but not limited to, rabbits, mice, rats, etc. to induce the production of sera containing polyclonal antibodies specific for the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species, and include but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and corynebacterium parvum. Such adjuvants are also well known in the art.

[222] Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies, or a combination thereof. For example, monoclonal antibodies can be produced using hybridoma techniques including those known in the art and taught, for example, in Harlow et al., Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: Monoclonal Antibodies and T-Cell Hybridomas 563-681 (Elsevier, N.Y., 1981) (said references incorporated by reference in their entireties). The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

[223] Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art and are discussed in detail in the Examples. In a non-limiting example, mice can be immunized with a polypeptide of the invention or a cell expressing such peptide. Once an immune response is detected, e.g., antibodies specific for the antigen are detected in the mouse serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells, for example cells from cell line SP20 available from the ATCC. Hybridomas are selected and cloned by limited dilution. The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding a polypeptide of the invention. Ascites fluid, which generally contains

high levels of antibodies, can be generated by immunizing mice with positive hybridoma clones.

[224] Accordingly, the present invention provides methods of generating monoclonal antibodies as well as antibodies produced by the method comprising culturing a hybridoma cell secreting an antibody of the invention wherein, preferably, the hybridoma is generated by fusing splenocytes isolated from a mouse immunized with an antigen of the invention with myeloma cells and then screening the hybridomas resulting from the fusion for hybridoma clones that secrete an antibody able to bind a polypeptide of the invention.

Another well known method for producing both polyclonal and monoclonal human B cell lines is transformation using Epstein Barr Virus (EBV). Protocols for generating EBV-transformed B cell lines are commonly known in the art, such as, for example, the protocol outlined in Chapter 7.22 of Current Protocols in Immunology, Coligan et al., Eds., 1994, John Wiley & Sons, NY, which is hereby incorporated in its entirety by reference. The source of B cells for transformation is commonly human peripheral blood, but B cells for transformation may also be derived from other sources including, but not limited to, lymph nodes, tonsil, spleen, tumor tissue, and infected tissues. Tissues are generally made into single cell suspensions prior to EBV transformation. Additionally, steps may be taken to either physically remove or inactivate T cells (e.g., by treatment with cyclosporin A) in B cell-containing samples, because T cells from individuals seropositive for anti-EBV antibodies can suppress B cell immortalization by EBV.

In general, the sample containing human B cells is innoculated with EBV, and cultured for 3-4 weeks. A typical source of EBV is the culture supernatant of the B95-8 cell line (ATCC #VR-1492). Physical signs of EBV transformation can generally be seen towards the end of the 3-4 week culture period. By phase-contrast microscopy, transformed cells may appear large, clear, hairy and tend to aggregate in tight clusters of cells. Initially, EBV lines are generally polyclonal. However, over prolonged periods of cell cultures, EBV lines may become monoclonal or polyclonal as a result of the selective outgrowth of particular B cell clones. Alternatively, polyclonal EBV transformed lines may be subcloned (e.g., by limiting dilution culture) or fused with a suitable fusion partner and plated at limiting dilution to obtain monoclonal B cell lines. Suitable fusion partners for EBV transformed cell lines include mouse myeloma cell lines (e.g., SP2/0, X63-Ag8.653),

heteromyeloma cell lines (human x mouse; e.g, SPAM-8, SBC-H20, and CB-F7), and human cell lines (e.g., GM 1500, SKO-007, RPMI 8226, and KR-4). Thus, the present invention also provides a method of generating polyclonal or monoclonal human antibodies against polypeptides of the invention or fragments thereof, comprising EBV-transformation of human B cells.

[227] Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, Fab and F(ab')2 fragments of the invention may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). F(ab')2 fragments contain the variable region, the light chain constant region and the CH1 domain of the heavy chain.

For example, the antibodies of the present invention can also be generated using [228] various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In a particular embodiment, such phage can be utilized to display antigen binding domains expressed from a repertoire or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 binding domains expressed from phage with Fab, Fv or disulfide stabilized Fv antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Examples of phage display methods that can be used to make the antibodies of the present invention include those disclosed in Brinkman et al., J. Immunol. Methods 182:41-50 (1995); Ames et al., J. Immunol. Methods 184:177-186 (1995); Kettleborough et al., Eur. J. Immunol. 24:952-958 (1994); Persic et al., Gene 187 9-18 (1997); Burton et al., Advances in Immunology 57:191-280 (1994); PCT application No. PCT/GB91/01134; PCT publications WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Patent Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

[229] As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')2 fragments can also be employed using methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al., BioTechniques 12(6):864-869 (1992); and Sawai et al., AJRI 34:26-34 (1995); and Better et al., Science 240:1041-1043 (1988) (said references incorporated by reference in their entireties).

Examples of techniques which can be used to produce single-chain Fvs and [230] antibodies include those described in U.S. Patents 4,946,778 and 5,258,498; Huston et al., Methods in Enzymology 203:46-88 (1991); Shu et al., PNAS 90:7995-7999 (1993); and Skerra et al., Science 240:1038-1040 (1988). For some uses, including in vivo use of antibodies in humans and in vitro detection assays, it may be preferable to use chimeric, humanized, or human antibodies. A chimeric antibody is a molecule in which different portions of the antibody are derived from different animal species, such as antibodies having a variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region. Methods for producing chimeric antibodies are known in the art. See e.g., Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Gillies et al., (1989) J. Immunol. Methods 125:191-202; U.S. Patent Nos. 5,807,715; 4,816,567; and 4,816397, which are incorporated herein by reference in their entirety. Humanized antibodies are antibody molecules from non-human species antibody that binds the desired antigen having one or more complementarity determining regions (CDRs) from the non-human species and a framework regions from a human immunoglobulin molecule. Often, framework residues in the human framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, preferably improve, antigen binding. These framework substitutions are identified by methods well known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual framework residues at particular positions. (See, e.g., Queen et al., U.S. Patent No. 5,585,089; Riechmann et al., Nature 332:323 (1988), which are incorporated herein by reference in their entireties.) Antibodies can be